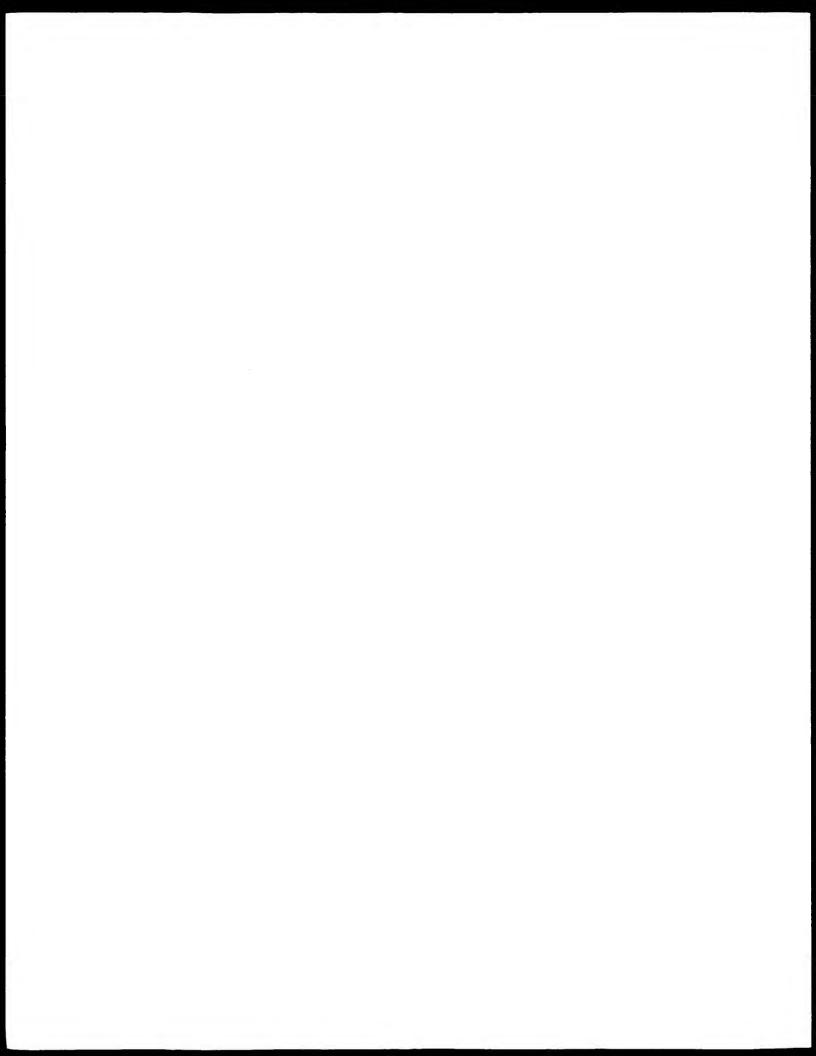
SEARCH REQUEST FORM

Scientific and Technical Information Center

Pequester's Full Name	Evaminer # .	Date:
Requester's Full Name: Art Unit: Phone Number 30 .	Serial Number:	Date.
Mail Box and Bldg/Room Location:	Results Format Preferred (circle):	PAPER DISK E-MAIL
If more than one search is submitted, please pri		
Please provide a detailed statement of the search topic, and des Include the elected species or structures, keywords, synonyms, utility of the invention. Define any terms that may have a spec known. Please attach a copy of the cover sheet, pertinent claim	, acronyms, and registry numbers, and co cial meaning. Give examples or relevant	ombine with the concept or
Title of Invention:		
Inventors (please provide full names):		
Earliest Priority Filing Date:		
For Sequence Searches Only Please include all pertinent inform appropriate serial number.	ation (parent, child, divisional, or issued pa	tent numbers) along with the

Jan Delaval Reference Librarian Biotechnology & Chemical Library CM1 1E07 – 703-308-4498 jan delaval@uspto.gov

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STAFF USE ONLY	Type of Search	Vendors and cost where applicable
SearcherA	NA Sequence (#)	STN
Searcher Phone #: 4466	AA Sequence (#)	Dialog
Searcher Location:	Structure (#)	Questel/Orbit
Date Searcher Picked Up:	Bibliographic	Dr.Link
Date Completed	Litigation	Lexis/Nexis
Searcher Prep & Review Time:	Fulltext	Sequence Systems
Clerical Prep Time:	Patent Family	WWW/Internet
Online Time: C/ 1	Other	Other (specify)



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Post-processing: Minimum March o%
Maximum Match 100%
Listing first 45 summaries
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

AUTHORS TITLE	REFERENCE	ORGANISM	SOURCE	KEYWORDS	VEPSION	ACCESSION	DEFINITION	rocus	AX259747	RESULT 1
Lorenz,M., Kriz,R., Weich,N. and Shaw,G.D. A p-selectin glycoprotein ligand (psgl-1) binding protein and uses therefor	Bukaryota; Metazoa; Chordata, Craniata, Vercebrata, Euteleostomi; Mammalia, Eutheria, Frimates, Catarrhini, Hominidae; Homo. 1	Homo sapiens	human.		AX259747 1 GI:16508816	AX259747	Sequence 1 from Patent W00173028.	AX259747 951 bp DNA linear PAT 26-0CT-2001		

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GENETICS INSTITUTE, INC. (US)
Location/Qualifiers
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YPRALELLLRVLPLQEKLTAHCPAAAVPALCAVLLCHRDLDRPAEAFAAGERALQRLQ
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Local Similarity 100.0%, Frcd. No. 5.1e-82,
hes 670; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                           CCAGCTCCGGAGGCCCACGCCCCGAGGCATCACTCTGAAGGAGCTCACTGTGCGAGAATA
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                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 16319)
Hugot, J P., Chamaillard, M., Zouali, H., Lesage, S., Cezard, J. I. Belaiche, J., Almer, S., Tysk, C., O'Morain, C.A., Gassull, M., Binder, V., Finkel, Y., Cortot, A., Modigliani, R., Laurent-Puig Gower-Rousseau, C., Macry, J., Colombel, J. F., Sahbatou, M. and Thomas, G.
                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                  HSA303140 163319 bp INA linear Homo sapiens NOD2 gene for LRR-containing protein, AJ303140 GI.14488148 LRR-containing protein; NOD2 gene.
Association of NOD2 leucine-rich repeat susceptibility to Crohn's disease
                                                                                                                                                                                         human
                                                                                                                                   Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                 variants with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature
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ATWANGLAAFLLOHVQELPVPLALPELEAATCKKYMAKLTTTVSAGSRFLSTYDGAET
LCLEDITTENVLEVWADVGMAGSPQKSPATLGLEELFSTFGHLNDDADTVLLVGEAGS
GKSTIL.QRIHLLMAAGQDPGEFLFVFPSCROLOCMAKPLSVRTLLFEHCCMPDVGQE
DIFQLLLDHPDRVLLTFDGFDEFKFRFTDRERHCSPTDPTSVQTLLFNLLQGNLLKNA
RKVVTSRPAAVSAFLRKYIRTEENLKGFSEQGIFELYLFKFHREFGYNADRLIFBLLOETS
ALHGI_CHLPVFSWMYSKCHQELLLOEGGSFKTTTDMYLLILDHFLLHATPPDSASQGL
GPSLLRGRLPTLLHIGRLALWGLGMCCYVFSAQQLQAAQVSPDDISLGFLVRAKGTVP
GSTAPLEFILHITPCCFFAAFYLALSADVPPALLRHLFNCGRPGNSPMARLLPTMCTQA
SEGKDSSVAALLQKAEPHNLQITAAFLAGLSREHWGLLAGCQTSEKALLRRQACABW
CLARSLPYLHFHSI IPDAAPCEAKSYHAMPGFTWLIRSLYEMQGEEPLAPVAAPCINVSHL
KLTFCSVGPTECAALAFVLQHLRRPVALQLDYNSVGDIGVEQLLPCLGVCKALYLRON
NISDRGICKLIECOLHCEQLOKLALFUNKLTDGCAHSMAKLACRQNFLAIRLGNNYI
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NISDRGICKLIECOLOKLALFUNKLTDGCAHSMAKLACRQNFLAIRLGNNYI
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NISDRGICKLORGHNAKLTDGCAHSMAKLTDGCAHSMAKLAGRUNYI
NISDRGICKLORGHNAKLTDGCAHSMAKLTD
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121552...121635,122230...123313,124418...124501,
128745...128828,130674...130746)
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/protein_id="CAC42117.1"
/db_xref="GG:14488149"
/translation="MCSOEAFQAORSQLVELLVSGSLEGFESVLDWLLSWEVLSWEDY
EGFHLLGOPLSHLARRLLDTVWNKGTWACQKLIAAAOEAQADSQSPKLHGCWDPHSLH
115601, .115820
/gene="NOD2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAAGAQVLAEGLRGNTSLQFLGFWGNRVGDEGAQALAEALGDHQSLRWLSLVGNN1GS
VGAQALALMLAKNVMLEELCLEENHLQDEGVCSLAEGLKKNSSLK1LKLSNNC1TYLG
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98302. .9890
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121552 1121635,122230 122313,124418 124501,
128745 128828,130674 131094)
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/db_xref="taxon:9606"
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/gene="NOD2"
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/gene="NOD2"
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This entry has been annotated with sequence quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (20-MAY-1999) Center for Human Genome Studies, District for Blamos National Laboratory, MS M888,
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Bruce, D., Mundt, M., Doggett, N., Munk, C., Saunders, E., Robinson, D., Jones, M., Buckingham, J., Chasteen, L., Thompson, S., Goodwin, L., Jones, M., Buckingham, J., Meinoke, L., Longmire, J., White, S., Tatum, O., Bryant, J., Tesmer, J., Meinoke, L., Longmire, J., White, S., Tatum, O., Campbell, C., Fawcett, J., Maltbie, M., Bussod, M., Sutherland, R., McMurry, K., Han, C. and Deaven, L.
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Homo sapiens chromosome 16 clone RPI1-401P9, complete sequence.
AC007608
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DOE Joint Genome Institute.
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Alamos, NM 87545, USA
3 (bases 1 to 16973)
DOF Joint Genome Institute.
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DOE Joint Genome Institute.
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  This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to qual:
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Hase-by-base quality values are not generally visible from the GenBank flat file format but are available as part
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/db_xref="taxon:9606"
/chromosome="16"
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                                                                               GAGAGGTTGAGAGGGAGGTCCTCAAGCGCTTCGGAGCTGGAGCTGGAGGACGTGGCGTTC
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/db_xref="G:114719305"
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/translation="MASRPHPGSPGWPGPINQCPTPTPQEVLPPGPDLPCPGPEEAQD
/translation="MASRPHPGSPGWPGPINGCPTPTPQEVLPCPGPDLPCPGPEEAQD
GPSSNSSMTTPELQEHWQKEKSRWKHVRLLFEIASARIEERKVSKFVMYQVVVIQTGS
GPSSNSSMTTPELQEHWQKEKSRWKHVRLLFEIASAFTITGENPALELLGALLGHEDGELTAR
GPSAAVPARCVAVPSPEEDLFTTPPELJEBAFGCTARAGGYAALELLGALLGLOGKLTAR
YLRLLYAVRAVPSPEEDLFTTPELJEBAFGCTARAGGYAALELLGALLGLOGKTAAL
CPSAAVPALCAALVCLFDLERPAEAFAVGEPALPCLFTPENHPYYAPLLDAMVPLAYA
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/strain="C57BL/6J"
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                                                                                      Submitted (05-JJL-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA.
On Jul 5, 1001 this sequence version replaced girllo72256.
                                                                                                                                                                Parkway, St. Louis, MO 63108, USA 3 (bases 1 to 260755)

McFherson, J.D. and Waterston, R.H.
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AC126054.2 GI:21699729
HTG; HTGS_PHASEI; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            250/755 bp DNA linear HTG 05-J
Mus musculus chromosome UNK clone RF23 298013, WORKING DRAFT
SECUENCE, 24 unordered pieces.
AC126054
                                                                                                                                                                                                                 Direct Submission
Submitted (92-JH, 2002) Geneme Sequencing Center, 4444 Forest
                                                                                                                                                                                                                                                            2 (bases 1 to 260755)
McPherson,J D and Wat
                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 260755)
McPherson, J.D. and Wat
                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
                                                                                                                                                                                                                                                                                                                     The sequence of Mus musculus
Web site:http://genome.wustl.edu/gsc/index.shtml
                     Center code: WUGSC
                                     Center: Washington University Genome Sequencing Center
                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                     house mouse
                                                        ---- Genome Center --
                                                                                                                                                                                                                                                                                                                                       and Waterston, R.H.
                                                                                                                                                                                                                                                              and Waterston, P H
                                                                                                                                                                                                                                                                                                                     clone
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Sequencing

Center project name. M_BA0298013 Contact. submissions@watson.wustl.edu

Project Information -----

Sequencing

vector. vector:

plasmid; 100%

Summary Statistics

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Chemistry: Dye-primer ET; 0% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 247976 bases at least Q40 Consensus quality: 250213 bases at least Q30 Consensus quality: 251775 bases at least Q30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality coverage: 0.00 in Q20 bases; agarose-fp Quality coverage: 8.85 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Insert size: 202000; agarose-fp
Insert size: 258455; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: This is a 'working draft' sequence. It currently consists of 24 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        as soon as it is available and the accession number will be preserved.
              /chromosome="UNK"
/clone-"RP23-298013"
1. .1038
                                                                                                                                                                              Location/Qualifiers
                                                                                             organism="Mus musculus"/db_xref="taxon:10090"
                                                                                                                                                                                                                                                          95442: gap of unknown length
116513: contig of 21471 bp in length
116613 gap of unknown length
137947: contig of 21334 bp in length
138047: gap of unknown length
164667: contig of 26620 bp in length
164667: gap of unknown length
204254: contig of 39487 bp in length
204254: contig of 39487 bp in length
204354 gap of unknown length
204354 gap of unknown length
204354 contig of 55069 bp in length
                                                                                                                                                       .260755
                                                                                                                                                                                                        259423: contig of 55069 bp in length 259523: gap of unknown length 260755. contig of 1232 bp in length.
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1138: gap of unknown length
2235: contig of 1097 bp in length
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of unknown length
ig of 11427 bp in length
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of 2692
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of 2684
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of 1558
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259524. .260755
/note="assembly_name:Contig8"
63869 c 62878 g 64428 t
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95043 . .116513
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1139. .2235
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164768. .204254
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138048. .164667
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116614. .137947
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16747. .19438
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JOURNAL REFERENCE

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                                                                                                                                                                                                                                                                                                             Submitted (24-007-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomicswhri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) MEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research institute (HRI) (supported by Japan Key Technology Center etc.); 5' & 3' end one pass sequencing. RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: RAB and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tashiro, H., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Watsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T. Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T. Nagahari, M. Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T.
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Isogai, T. Orsuki, T
Direct Submission
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Homo sapiens kidney cDNA to mRNA, clone_lib:KIDNE2
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                                                 /db_xref="taxon.9606"
/clone="KIDNE2006353"
/tissue_type="kidney"
                                                                                                                                     /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                    Submitted (30-JUN-2001) Membrane Biology Laboratory, Institute Mol & Cell Biol, 30 Medical Drive, Singapore 11/609
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                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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            SGPDRFLLTLAGLAVCHOELED#GEARACCEKALQLLGDKSLHPLLAPFLEAHVRLSW
RLGLDKRQSEARLQALQEAGLTPTPPPSLKELLIKEVLD"
                                                               /clone_lib="KIDNE2"
/note="cloning vector: pME18SFL3"
a 919 c 790 g 775 t
                                                FLGHLQAVPELRHAPDLQDFFVLPELRRAQSLTCTGLYREALALWANAWQLQAQLGTP
                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                       /note="member of sorting nexim protein family"
/codon_start=1
/product="SNX21"
                                                                                                                                     /protein_id="AAK73126.1"
/db_xref="GI:14719307"
                                                                                                                                                                                                                                                                                                                  organism="Homo sapiens"/
                                                                                                                                                                                                                            'yene="SNX21"
                                                                                                                                                                                                                                                              gene="SNX21"
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Direct Submission
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/protein_id="AAM77915.1"
/db_xref="G1:21866801"
/translation="MHR97955AMASPILHFI.PHALA95GPGEAAASPEAEGFPESSE
LEDDDAEGLSSRLSGTLSFTSAFDIEDDEDEDEDEAGPDQLFLGDGTSGLIAERS.PPP
DGOWGSQLLARQLQDFWKKSRTLAPGRLLFBVTSAHDLFDWSTVYUYTTALAVIGPGP
DGOWGSQLLARQLQDFWKKSRTLAPGRLLFBVTSAHDLFDFWFUFPPSRAFED
DCQDAQISPPYSDEEPLHPMLQDGPGPMALSFTTGLYREALALWARAWLAWQLJGTG
PDCQPAQISPPYSDEEPLHPMLQDGFBARACCEKALQLLGDKSLHPLLAPFLEAHVRLSW
SGPDRRPLTLAGLAVCHQELEDPGBARACCEKALQLLGDKSLHPLLAPFLEAHVRLSW
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Submitted (15-MAY-2001) E-mail contact humquery@sanger ac.uk

Submitted (15-MAY-2001) E-mail contact humquery@sanger ac.uk

This cDNA sequence was assembled from public domain ESTs and single

pass sequencing reads from expressed DNA templates, aligned to the

genomic DNA sequence from the bacterial clone 337018 (AL008726).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The EST sequences listed match this sequence with an identity of at least 95% between the coordinates shown.
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FLGHLQAVPELPHAPDLQDFFVLPELPRAQSI.TCTGI.YPFALALMANAWQI.QAQLGTP
SGPDRPLI.TLAGLAVCHQELEDPGEARACCEKALQLI.GDKSI.HPLI.APFLEAHVRLSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start_1
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/product="hypothetical protein"
/proviein [il="CAC 39140 1"
/db_xref="GI:1414 9068"
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LEDDDDAEGLSERLSGTTLSETTSAEDDEDDEDEDDEAEAGPDQLPLGDGTGSGEDAERSPPP
DCOWGSQLLARQLQDFWKKSRNTLAFQRLLFEVTSANVVKDPESKYVLYTLAVIGEGP
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join(15. .446,447. .515,515. .540)
/note="matches EST BE778315 from clone IMAGE:1866880"
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/note="matches EST BF115410 from clone IMAGE:3570963"
                                    join(529. .679,763. .784)
/note="matches EST T73159 from clone IMAGE:85952"
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                                                                                                                                                                                                        354. .517
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170 | GGCGGGAGCTTCAGCAGTACTGACAGAACCAGAACCAGTGAAACGAGTGAAACGACGTGAAACTGC | 229
703 GTAGCC9930^TTTT8A9CASTTTTTP993TCACCT9CA99CA3TGCTT5A9CTP3C9CCATS 762
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/note="matches EST BF061958 from
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/note="matches EST AI400589 from clone IMAGE:2115843"
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Pred. No. 9.6e-13;
0; Mismatches 317;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Habib Zouali
Inflammatory Bowel Diseases
Centre d'Etude du Polymorphisme Humain (CEPH)
27, rue Juliette Dodu 75010 Paris, France
Tel: 00 33 1 53 72 50 20
Fax: 00 33 1 53 72 50 58
Email: habib@cephb.fr
Primer A: GGAAGCAGAGTGAAAGAGG
Primer B: GGCATCTCCCCAAGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCTCCTGGCGCCTGGGCCTGGAC 1085
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            Unigene EST cluster hs.87280; This STS contains a coding sequence which was identified by screening of Human cDNA library.

Location/Qualifiers
                                                                                                                          Buffer:
Tris-HCl
                                                                                                                                                                                                                                                                                                                                                                   activate AmpliTaq Gold, 30 cycles: 94 degrees C for 30 sec, annealing for 30 sec at 55 degrees C, extension at 72 degrees C for 30 sec; last extension at 72 degrees C for 7 min.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Association of NOD2 leucine-rich repeat variants with susceptibility to Crohn's disease Nature 411 (6837), 599-603 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STS size: 270
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1 (bases 1 to 270)
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667944
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IBDlprox-exonC genomic STS on chromosome 16q12-13 Homo sapiens
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             249 TCGCATCGAGGAGAGAAAAGTCTCTAAGTTTGTGGT 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        140 CTGGCAGAACCAGAAATGCCGCTGGAAGCACGTCAAACTGCTCTTTGAGATTGCTTGAGC
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                                                                                                                                                                                                                        Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan (B-mail:genomics%hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NBDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan, cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tanigami,A., Fujiwara,T., Shibahara,T., Goto,Y., Hirao,M., Shimizu,F., Wakebe,H., Ono,T., Hisbigaki,H., Waranahe,T., Oraki,K., Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y., Satto,K., Nishikawa,T., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M., Kiwuchi,H., Kanda,K., Wagatsuma,M., Murakawa,Y., Kanehori,K., Kiwuchi,H., Kanda,K., Wagatsuma,M., Murakawa,K., Kanehori,K., Takahashi-Fujii,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  oligo capping; fis (full insert sequence).

Homo sapiens chondrocytes (HC) cDNA to mRNA, clone_lib.HCHON2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3044 bp mRNA linear
Homo sapiens cDNA FL719532 fis, clone HCHON2001099,
AK095851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 3044)
Isogai,T. and Yamamoto,J.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone: HCHCN2001099.
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/note="Genomic STS were identified on Human CEPH-BAC clone (hbs7b10) located on chromosome 16 using shot-gun and sequencing procedures."
                              /clone="HCHON2001099"
/cell_type="chondro---
/cell_type="chondrocytes (HC)"
/clone_lib="HCHON2"
                                                                                                       /db_xref="taxon:9606"
                                                                                                                                                                                                    Location/Qualifiers
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Pred. No. 7.5e-12;
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DEFINITION
ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                      TGCTTCGGGACAAGAGCCTCCACCCTTTBGCTGGCACCCTTTTCTGGAGGCCCATGTCCGGC
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                                                                      Homo sapiens cDNA FLJ34040 fis, clone FCBBF2005966 AK091359
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DLQDFFVLPELPRAQSLTCTGLYPEALALWANAWQLQAQLGTPSGPDPDLTLAGLAV
CHQELEDPGEAPACCEKALQLLGNKSLHPLLAPFLEAHVPLSWAFEQFLGHLQAVPELPHAP
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/db_xref="GI:21755195"
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Pred. No. 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tesno, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Fimira, K., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Fimira, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K., Kagatsuma, M., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Suruki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T., Nagai, K. and Isogai, T., Nagai, K. and Isogai, T., Nagai, K., Nagai,
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Homo sapiens fetal brain cDNA to mRNA, clone_lib:FCBBF2
clone:FCBBF2005966.
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Direct Submission
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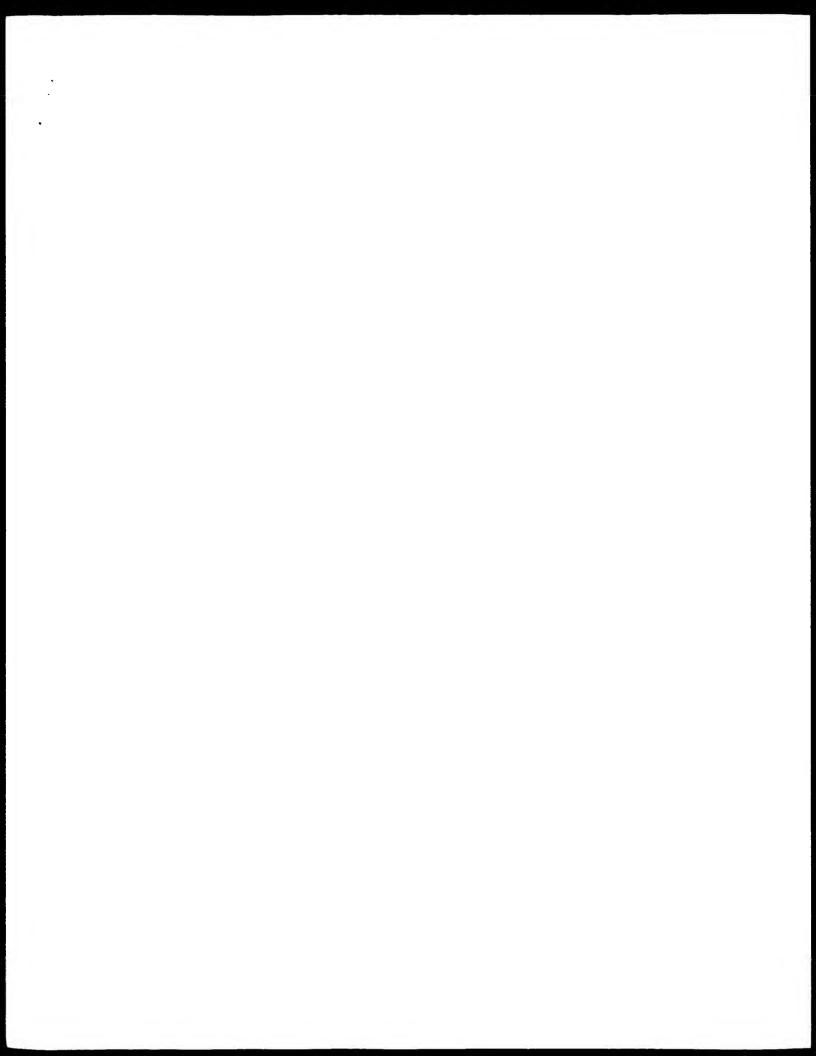
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Submitted (18-APR-2000) National Laboratory For Oncogenes Genes, Shanghai Cancer Institute, 25/Ln 2200 Xie-Tu Road, 200032, People's Republic of China
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1 (Dases 1 to 2064)
Prin_W X. Zhou.X M , Zhang,P P., Jiang,H.Q., Huang,Y , Wan,C.F
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Search completed. April 20, 2003, 15:50:04 Job time: 5691 secs



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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		Query				
No.	Score		ength	В	\vdash	Description
p ;	693.8	73.0	1	14	BQ706954	BQ706954 AGENCOURT
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5032 am41e07.	3915 on91c11.	6379	3303 op46f12.s	01659 ug88h12.	16883 TCAAP1	25558 us17h05.	93158 TCBAP1E1	15468 BB6454	2215 ob78h12.	1579 oc84f06.	2390 zs89a11.	2085 cp76e12.	3472 td06h05.	19874 TCAAP3E	94142 TOWAPIQI	0235 tm26a01.	1511 al56h02.	71924 EST3840	3920 ou41b04.	94126 TUAAFI	3706 zs77c05.	92328 tq66g07.	21424 Ja69all.	09178 oll2a07.s	C	24066 ah98£02.	07226 cc36g04.s	409523 6029639	1მაგლის ნიხ7	4174 te50d05.x	463821 hd35£08	1560 qb82d04	4170 th10a08.	92491 hf43cll	243205 qh40h06	6 60288	004982 ou07a09.x	W467091 ha0

ALIGNMENTS

FEATURES source		COMMENT		AUTHORS	REFERENCE		MSIN	SOURCE		ACCESSION		ITION		BO706954	1
High quality sequence stop: 567. Location/Qualifiers 1934	Email: cgapbs-r@mail.nih.gov Tissue Procurement: Dr. Mark Watson cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov	Contact: Robert Strausberg, Ph.D.	National Institutes of Health, Mammalian Gene Collection (MGC)	NIH-MGC http://mgc.nci.nih.gov/.		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens	EST.	BQ706954.1 GI:21845853	BQ706954	5', mRNA sequence.	T_8353554 NIH MGC 113 Homo sapiens cDNA clon	RO706954 934 br mpNb linear EST 16-III - 2002		

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                                                                                                              | CCTGGACTTCCTTANTSCASTORAGATETOSCASTASTTTTCGASTTGCCTGCCGASGCGA 599
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/db_xref="taxon:9606"
/clone="IMAGE:6279494"
/clone=imyMagE:6279494"
/clone=imyMagE:6279494"
/clone=ib="NIH MGC 113"
/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: proms; Site 1: XhoI; Site 2:
/coRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies) Note: this is a NIH MGC Library."
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90.6%;
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GCTTCAGCTCGCATCGAGGAGAGAGAAAAGTCTCTAAGTTTGTGGTGTTACCAAATCATCGTC
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC Clone distribution information can be
found through the I M A G E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 643.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases : to 772)
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Similarity 99.9%;
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/clone="lb4"NTH MGC 92"
/tissue_type="embryonal carcinoma, cell line"
/lab host="DH10B (phage resistant)"
/note="Organ. testis, Vector. pCMV-8PORT6, Site_1: Not1;
Site_2: Sall, Cloned unidit="tionally: oligo-dT primed.
Average insert size 2.5 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NHH MGC Library."
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                                                                          Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system-J84-format sequencing pipeline with 384 multicapillary sequencer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes fenome Pes 10 (10), 1617 1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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                           Genome Res. 10 (11), 1757-1771
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                                                                                                                                                                                                                                                                  CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rike Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fax:81-45-503-9216) Please visit our web site (http://genome.gsc riken.go jp/) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yo
Kanagawa 230-0045, Japan (E-mail genome-res@ysc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Pesearch (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC)
                                                                                                                                                                                                                                                                                                                                                                                                                                   Rot = 185.2. Second strand cDNA was prepared with the primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                              prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGAGATCCAAGAGCTCTTTTTTTTTTTTTVN 3'], cDNA was
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             /strain="C57BL/6J"
/db_xref="PANTOM_DB:9130017C17"
/db_xref="MGD:MGI:1904167"
/db_xref="Maxon:10090"
/clone="9130017C17"
                                                                                                                                                                             /organism="Mus musculus"
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                                                      ATCEAGACTGGAGACTTTGGACAACAACAAGGCCGTCCTGGAACGGCGCTATTCCGACTTC 360
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                                   CACTGCCCGAGCGTTTGCGCCGCGCGCGCTCTTGCGCGCGACCTC 874
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="cecum"
/clone_lib-"RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
164._.1105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="BAB31317.1"
/db_xref="GI:12858438"
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79.4%;
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Pred No 1.9e-116;
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UI-H-BI1-abs-e-09-0-UI sl NCI CG
IMAGE:2713048 3', mRNA sequence.
AW134842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oligo-dT track not found, Not I site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D. Email. cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata; Vertebrata; Eutéleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 567)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCT-CGAP http://www.ncbi nlm nih gov/ncicgap
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              information can be found through the I.M.A.G.E. Conscrtium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumor Gene Index
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                                                                                                                                                                                                                     /lab host="DHIOB (Life Technologies)"

/note="Weetcor: pTTT3D-Pac (Pharmacia) with a modified polylinker, Site=1: Mot 1; Site=2: Ecc R; The NCI CGAP Sub library is a subtracted library derived from the MCI CGAP Sub1 library is a subtracted library derived from the MCI CGAP Sub1 library, which is a subtracted library derived from BI. BI constitutes a mixture of 21 derived from BI. BI constitutes a mixture of 21 rormalized or subtracted NCI CGAP Kid1; NCI CGAP Kid2, NCI CGAP Kid1; NCI CGAP Kid1; NCI CGAP Kid1; NCI CGAP Kid1; NCI CGAP Kid2, NCI CGAP Kid3, NCI CGAP Kid3, NCI CGAP Kid4; NCI CGAP Lu24, NCI CGAP Brn23, NCI CGAP Lu24, NCI CGAP Brn25. These 21 libraries were pooled and a single-stranded DNA preparation of the resulting mixture was used as a tracer in a subtractive hybridization with a Arrivar where resulting mixture was used as a tracer in a subtractive hybridization with
/db_xref="taxon:9606"
/clone="IMAGE:2713048"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone_lib="NCI_CGAP_Sub3"
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                                                                                                                                                                                                                                                                                                              AGCTCACCGCCACTGCCCTGCGGCCG 676
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eurheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 540)
                                                            Homo sapiens
                                                                                                                                                                    wg97a05 x1 NCI_CGAP_Kidii Homo
                                                                                                                                      mRNA sequence.
AI762326
                                                                                                                      AI762326.1 GI:5177993
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LLAM 2457-2459, 2758-2759, 3062-3068 [TMAGE CloneIDs
985068-986759, 101192-1101959, 121928-1220615),
NCI_CGAP_Colo pool 1
LLAM 2644-2653, 2871-8872 [TMAGE
CloneIDs 1057416-1061255, 1144984-114535]. Subtraction
was performed as previously described [Bonaldo, Lennon &
Soares (1996): Normalization and Subtraction: Two
Approaches To Facilitate Gene Discovery. Genome Research
6, 791-806.
TAG_LIB=NCI_CGAP_Lu5
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175 g 115 t
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                                                                                                                                                                      p mRNA linear EST 20-DEC-1999
sapiens cDNA clone IMAGE:2379152 3',
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GGGASCTTCAGCAGTACTGGCAGAACCAGAAATGCCGCTGGAAGCACGTCAAACTGCT
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                                                                                                                                                                                            TGGAGTTTCCCAGGAAGCACCTGACTGGGAACTTCGCTGAGGAGATGATCTGTGAGCGTC
                                                                                                                                                                                                                                                                                                                               TCATCCTCACAGA/TGGGGACTTTGA/AA/AA/AA/AA/GCGTCCTGGAACGGCCCTATT
                                                                                                                                                                                                                                  CCGACTTCGCGAAGCTCCAGAAAGCGCTGCTGAAGACGTTCAGGGAGGAGGATCGAAGACG 241
                                                                                                                                                                                                                                                                                                                                                                                        TTGAGATCGCTTCAGCTCGCATCGAGGAGAGAGAGTCTCTAAGTTTGTGGTGTACCAAA
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
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Contact: Robert Strausberg, Ph.D.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.,
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/clone="IMAGE:2379152"
/clone_lib="NCI_CGAP_Kidl1"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                  184 CAGTACTGGCAGAAACGAGAAATGGCGGCTGGAAGGAGGTGCTGTTTGAGATGGGT 243
                                                                 304 CAGACTGGGAGCTTTGACAACAACAAGGCCCTCCTGGAACGGCGCTATTCCGACTTCGCG 363
$64 MOCTOCAGAAAGAA TOCTGAAGAAATTTAAAAGAATATAAAAAAAAGATGTGAAGTTTTCCC 423
                                           349 CAGACTEGGAGCTTTGACAACAACAAGGGCGTATTCCCACTTCGCG 290
                                                                                                                                                                                                                                                                                                                                                                                                                                           ocal Similarity
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                                                                                                                                    TCAGCTCGCATC (ACA)ACAAAAACTCTCTAAGTTTGTGGTGTACCAAATCATCGTCATC 350
                                                                                                                                                                                                                                                                                                                                                                                                                       528;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Possible reversed clone: polyT not found Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
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Location/Qualifiers
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Seq primer: -40UP from Gibco
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Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1997)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Emmert-Buck, M.D., Ph.D.
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                         purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (closes 1323912-1325831, 1471366-1472903 and 1492104-1493255). Subtraction by Bento Soares and M. Fatima Bunaldo. "
                                                                                                                                                                       /note="Organ: kidney; Vector. pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1. Not 1, Site 2. Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Kid5 was
                       Fatima Bunaldo.
                                                                                                                                                         prepared, and ss circles were made in vitro. Following HAP
                                                                                                                                                                                                                                             /clone="IMAGE.2873213"
/clone_lib="NCI CGAP Kid12"
/tissue_type="2 pooled tumors (clear cell type)"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
    157 c
149 g
    104 t
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Best Local Similarity Matches 504, Conserv

Conservative

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Mismatches

51.7%;

Score 491.8; DB 1 Pred. No. 8.2e-90;

DB 10; Length 506;

Galus

Query Match

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ou07a09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:1625560 3', mRNA sequence.
                                                                                                                                                                                                                                  This clone is available royalty-free through LLNL; contact the IMAGE Consortium (infedimage.llnl.gov) for further information. Insert Length: 791 Std Error: 0.00 Seg primer: primer name ambiguous.
                                                                                                                                                                                                                                                                                                                                                       Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                        NCT-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
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Mammalia; Eutheria;
1 (bases 1 to 478)
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AI004982.1 GI.3214492
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/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NBHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and ss circles were made in
                                                                                                  /clone="IMAGE:1625560"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                              organism="Homo sapiens"
                                                                                                                                                            db_xref="taxon:9606"
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMIIll1 row: a column: 11
                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 671)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                               Mus musculus
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Pred. No. 2.1e-85;
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Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image linl gov) for further information.
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AI243205
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/clone="IMAGE:1847195"
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                                                                                                                                                                                                                                                                                                                                                                                                          193 CASAACCAGAAATGCCGTETJSAAGCACGTECAAACTGCTCTTTTGAGATCGCTTCAGCTCGC 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
CTGACTGGGTAACTTCGGT5AGGAGGTACTGTGAGGGTCGGCGCCCCTGCAGGAGTAC 422
                                                                           AAASOSOTTOOTSAAGAOGTTOOASSAGAGAGAGAGGTOGAGGTTTCCCAGGAAGCAC 221
                                                                                                                  AAAGCGCTGCTGAAGACGTTCAGGGAGGGGAAGGATCGAAGACGTTGGAGTTTCCCAGGAAGCAC 432
                                                                                                                                                                                    AGCTTTGACAACAACAAGGC
                                                                                                                                                                                                           AGCTTTGACAACAACAAGGCCSTCCTGGAAACGGCGCTATTCCGACTTCGCGAAGCTCCAG 372
                                                                                                                                                                                                                                                                             ATCGAGGAGAAAAGTCTCTAAGTTTGTGGTGTACCAAATCATCGTCATCCAGACTGGG 341
                                                                                                                                                                                                                                                                                                                            ATCGAGGAGAGAAAAGTCTCTAAGTTTGTGGTGTACCAAATCATCGTCATCCAGACTGGG 312
                                                                                                                                                                                                                                                                                                                                                                             CAGAACCAGAAATGCCGCTGGAAGCACGTCAAACTGCTCTTTGAGATCGCTTCAGCTCGC 401
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460 bp mPNA linear ES: hf43c11.x1 Scares_NFL_T_GEC_S1 Homo sapiens cDNA clone IMAGE.2934644 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Possible reversed clone: polyT not found
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1 (bases 1 to 460)
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National Cancer Institute, Cancer Genome Anar
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/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
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                                                                           460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
M.D., Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M. Bento Scares, Ph.D.
cDNA Library Preparation: M. Bento Scares, Ph.D.
DNA Sequencing by: Washington University Benome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 795 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 460.
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                                                                                            Similarity
                                                                                                                                                                  88
                                                                         Conservative
                                                                                                                                                            /clone_lib="NCI_CGAP_CLL1"
/tissue_type="B-cell, chronic lymphotic leukemia"
                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:9606"
/clone="IMAGE:2117846"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                  /lab_host="DH10B"
                                                                   48.4.,
100 0%; F;
0;
                                                                     48.4%, Score 460; DB 9,
100 0%; Pred No. 2 2e-83;
Live 0; Mismatches 0;
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sapiens cDNA clone IMAGE:2117846 3',
                                                                                                          Length 461;
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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOCTCTACGCCATCCGCTGCGGCGCCGCTCCCGGGAGTTCCTGGACTTCCTCACGCGGGC 559
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A11:11560 mRNA linear EST 14-SEP-1998 db82004.xl Soares fetal heart_NbHH19W Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                         This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40m11 fwd ET from Amersham High quality sequence stop: 442.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCT-CGAP http://www ncbi nlm.nih gov/ncicgap
National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact · Pobert Strausberg, Ph.D.
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(Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung
                                                                    double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified p773 vector (Pharmacia). Library went through and account of the Not I and Eco RI sites of a modified p773 vector (Pharmacia).
                                                                                                                                                    /dev_stage="19 weeks"
/lab_host="DH19B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                        /sex="unknown"
                                                                                                                                                                                                                                                                                                     /clone="IMAGE:1706599"
/clone=lib="Soares_fetal_heart_NbHH19W"
/correstation="Soares"
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AUTHORS
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450 bp mRNA linear ES.
hd35f08.xl Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:2911527 3', mRNA sequence.
                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image_llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Geneme Anat
                                                                                                                                                                       High quality sequence stop: 408.
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/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
/note="Organ: pooled, Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Ecc RI;
                                                                           /db_xref="taxon:9606"
/clone="IMAGE:2911527"
                                                                                                                                                   Location/Qualifiers
                                                                                                                  organism="Homo sapiens"
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al Similarity 99.6%;
457; Conservative
                 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 838 Std Error: 0.00
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re50d05.x1 Soares_NFL_T_GBC_S1 Homo
IMAGE:2090121 3', mRNA sequence.
                                                                                                                                                                                                                                               Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria; Primates; Catarrhini, Hominidae; Homo.

(bases 1 to 500)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
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Seq primer:
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-40UP from Gibco
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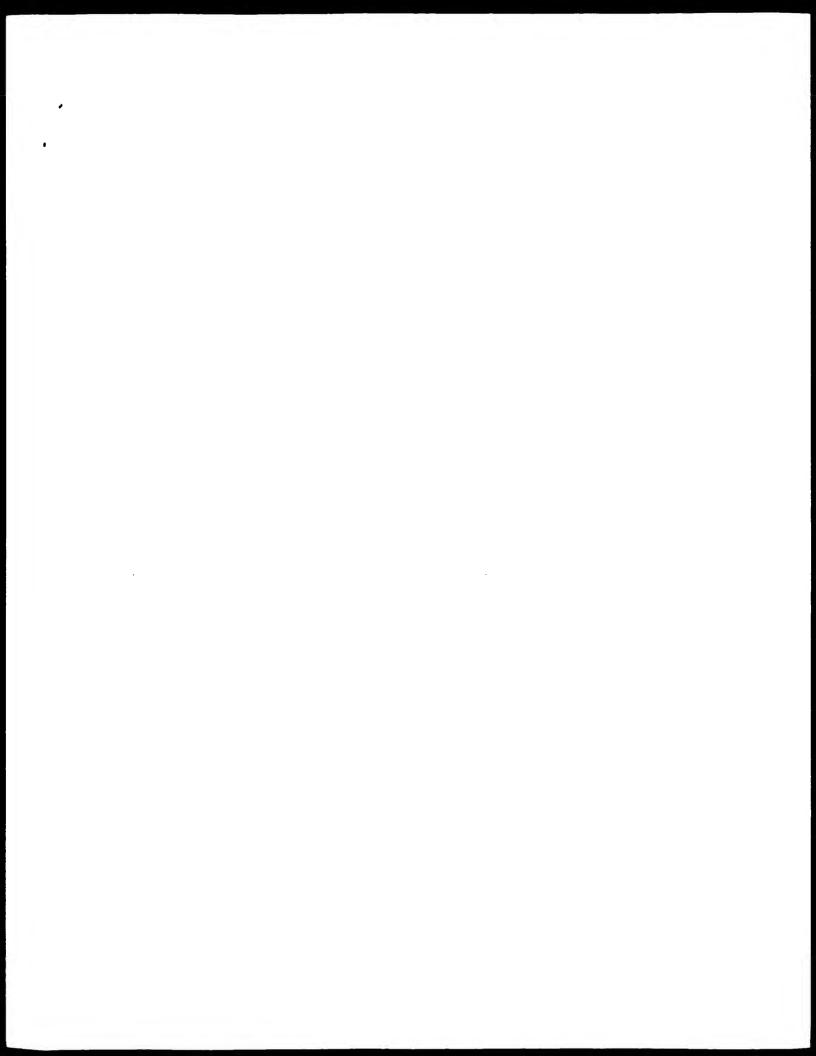
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SOURCE KEYWOPDS VERSION

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Best Local Similarity
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                                                           AGATCGCTTTCAGCTCGCATCGAGGAGAGAGAAAGTCTCTAAGTTTGTGGTGTACCNAATC
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Pred. No. 3.8e-82;
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

951 100.0 951 22 AAI65832 Nucleotide sequenc 949.4 99.8 1315 22 AAI65593 Nucleotide sequenc 817.6 86.0 1317 23 AAS84164 Nucleotide sequenc 670 70.5 8135 22 AAI65593 Nucleotide sequenc 506 53.2 806 23 AAS7873 DNA encoding novel
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		Gallus domesticus		domesticus	contai	tenolide	{s	Kidney cancer rela	Streptomyces roseo	yces fi	Zea	Collagen-like poly	Collagen-like poly	Micromonospora DNA	Drosophila melanog	Human herpesvirus	HSV 2 immediate ea	Streptomyces nours	Streptomyces nours	herpesv	HSV 2 strain SB5 C	strain S	yon g	Dia encoding novel	haem		nove	iffer	Human osteoblast d	mmune/haem	ic sequen	cancer cel	Human cancer cell		Human immune/haema

ALIGNMENTS

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03-JAN-2002 (first entry)
                                        AAI65832;
                                                                          AAI65832 standard; DNA; 951
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Nucleotide sequence of a human PSGL-1 binding protein.

Human, F selectin glycoprotein ligand binding protein;
PSGL-1 binding protein; selectin ligand interactor cyproplasmic-1 protein;
SLIC-1 protein; signal transduction; cytoskeletal organization;
immune response; inflammatory response; cell adhesion, cell migration;
cell activation; cell growth; cell differentiation; cell proliferation; immune system disorder; cardiovascular disorder; haematopoietic disorder; thrombotic disorder; ss.

Homo sapiens.

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ARESULT 1
AA165832
ID AA16
XX AA16
AC AA16
XX Nucl
XX Nucl
XX Huma
KW PSGLIC
KW Immu
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/*tag= a
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    binding protein"
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23-MAR-2001, 2001WO-US09469.

04-0CT-2001.

24-MAR-2000; 2000US-192104P

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PSGL 1) binding protein. The protein is a member of the selecting and interactor cytoplasmic (SLIC-1) family. The SLIC-1 polynucleotides and polypeptides are useful as targets for developing modulating agents to regulate a variety of cellular processes such as signal transduction, cytoskeletal organization, immune and inflammatory responses, interand intra-cellular communication, adhesion, migration, cell activation, growth, differentiation and proliferation. The SLIC-1 proteins provide movel diagnostic targets and therapeutic agents to control or modulate SLIC 1 molecule associated disorders such as an inflammatory or immune system disorder, a cardiovascular disorder, a cellular proliferation, activation, adhesion, growth, differentiation or migration disorder or a haematopoietic or thrombotic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated polynucleotides (SLIC-1) which encode novel P-selectin upper of the protein ligand (PSGL-1) binding protein, useful as targets for developing modulating agents to regulate a variety of cellular processes including signal transduction -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Fig 1; 108pp; English.
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                               CTGCAGGASTACCTBGGSCTBCTCTACGCATTSCGTGCGCGCGCGCGCGCGGGAGTTC 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence encodes a human P-selectin glycoprotein ligand
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 951; DB 22; 100.0%; Pred. No. 1.2e-166;
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                                                New human nucleic acids associated with intestinal inflammatory disease, useful for diagnosis, prognosis and control of these d
                                                                                                                                                                                                                                                                             Human; inflammatory bowel disease 1 protein; IBD1, IBD1prox; intestinal inflammatory disease; apoptosis; NF-kappa B; cancer; inflammatory disease, immune disease, cryptogenetic inflammation;
                       Claim 1; Page 72-73; 97pp; French.
                                        also related proteins
                                                                            P-PSDB; AAG79120.
                                                                                                                                        27 MAF-2000, 2000FR-0003832
                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                 Nucleotide sequence of IBD1prox protein.
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The present sequence encodes a human The IBD1prox protein is in preximaty

in preximaty to a gene enceding inflammatory

protein designated IRD1prox.

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1315 BP; 257 A; 419 C, 394 G, 245 T, 0 other,
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99.9%;
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                                 CC polypeptide (II) sequences. (II) is useful as hybridisation probes, and propertied (II) sequences. (II) is useful as hybridisation probes, and gene mapping, and in recombinant production of (II). The CC polymucleotides are also used in diagnostics as expressed sequence tags of or identifying expressed genes. (I) is useful in gene therapy techniques of or restore normal activity of (II) or to treat disease states involving CC (II). (II) is useful for generating antibodies against it, detecting or creations of the conditions of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1071
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P-PSDB; ABG19977.
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23-AUG-2000; 2000US-0649167.
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                    at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID No 19968; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAR-2001; 2001WO-US08631.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; chromoscme mapping, gene mapping, gene therapy, forensic; food supplement; medical imaging; diagnostic; genetic disorder;
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                                    GGAGGCCCACGCCCCGAGACATATCACCCCTSAAGAGAGCTCACTTGTGCGAGAATACCTTGCACT 949
                                                                                                                                                                                                                               CTACGCCCTGGGCAAGGACTTCGTGAACTCTGCAGGAGAGGCTGGCAGGAGGAGCCAGCTGC
                                                                                                                                                                                        CT-TCGCGAAGCTCC--AGAAAGCGCTGCTGAAGACGTTCAGGGAGGAGATCGAAGACGT 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GC-TTCACCTCGCATCGACAAAAGAAAAGTCTCTA-AGTTTGTGGTATACAAAATCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCTACGCGCTGGGCAAGGACTTCGTGACTCTGCAGGAGGGCTGGAGGAGAGAGCCAGCTCC 889
                                                                                                              CONTRACTOR TRACTACOTACOTACOTACOTACOTA ACCOCTOCOTACOCCOCOCOCOCO 530
                                                                                                                                                                                                                                                                                                                                                GGAGTTTTCCCAGGAAGAACACCTGACTGGGGAACTTCGCTGAGGAGATGATCTGTGCAGCGT 595
                                                                                                                                                                                                                                                                                                                                                            GGA-FTTT-UU-AGGAA-GUA-UUTGACT-GGGAACTTUGCTGAGGAGATGATCTGTG-AGCGT
                                                                                                                                                                                                                                                                                                                                                                                                                          GTCATCTCACACTS SCACCTTTSACAACAACAACAASCCCTCCTGGAACGGCGCTATTCCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                          GTCATC-CAGACTGGGAGGGCTTTTGACAACAACAAGGGCGTTCCTGGAAACGGCGGCTATTCCGA 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGCTTTCAPCTCGCATCGAGGAGAGAAAGTCTCTAGAGTTTGTGGTGTACCAAATCATC 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCAGCAGTACTSGCAGAAACGAGAAATGCCGCTGGAAGCACGTCAAACTGCTCTTTGAGAT 239
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P-PSDB; AAG79120.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, inflammatory bowel disease 1 protein, IBD1, IBD1prox; intestinal inflammatory disease; apoptosis; NF-kappa B; cancer; inflammatory disease; immune disease; cryptogenetic inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAI65594,
                                                                                                         New human nucleic acids associated with intestinal inflammatory disease, useful for diagnosis, prognosis and control of these d
                                                                                                                                                         Huget Jr,
                                                                                                                                                                                        27-MAF 2000, COOCER-0003832
                                                                                                                                                                                                       27 MAR-2000, 2000FR 0003822
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleotide sequence of IBD1prox gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-JAN 2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAI65594 standard; DNA; 8135 BP
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                                                                                                                                                         Thomas G,
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The present sequence encodes a human protein designated IBD1prox. The IBD1prox protein is in proximaty to a gene encoding inflammatory bowel disease 1 (IBD1) protein, which is associated with intestinal inflammatory disease. The IBD1 gene is probably involved in regulation of apoptosis and activation of NF-kappa B. The IBD1 and IBD1prox polynuclectides are is useful as source of probes and primers, as source of (anti)sense oligonucleotides, for recombinant production of polypeptides, and in screening for interactive compounds. The polypeptides are used to raise specific antibodies which useful for diagnostic detection or purification of IBD1 and IBD1prox, to screen

Claim 1; Page 75-77; 97pp; French.

also

related proteins

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RESULT 5
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AC AAS7
AC AAS7
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                                                                                                                                                                                                                                                                                      7872
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Human; chromosome mapping; gene mapping;
                                                                      13-FEB-2002
                                                                                                                                   AAS78753 standard; cDNA; 806
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                               DNA encoding novel human diagnostic protein #14557.
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                                                                                                                                                                                                                                                                                 CCASCTCCSSAGGCCCACSCCCCSAGGCATCACCCTGAAGGAGCTCACTGTGCGAGAATA
                                                                                                                                                                                                                                                                                                    CCAGCTCCGGAGGCCCACGCCCCGGAGGCATCACCCTGAAGGGAGCTCACTGTGCGAGAATA 941
                                                                                                                                                                                                                                                                                                                                                   CCGCCTGGCCTACGCGCTGGGCAAGGACTTCGTGACTCTGCAGGAGAGGCTGGAGGAGAG
                                                                                                                                                                                                                                                                                                                                                                          CCSCCTSGCCTACSCSCTSGGGAGAGACTTCGTGACTCTGCAGGAGAGCCTGGAGGAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              670;
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CC Note: The sequence data for this patent did not appear in the printed content types obtained in electronic format directly from WIPO cat fire wino int/pub/published for sequences.
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 806 BP; 169 A; 265 C; 239 G; 133 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1, SEQ ID No 14557; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-MAR-2000;
23-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              food supplement; medical imaging; diagnostic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                     116
240 CGC-TTCAGCTCGCATCGAGGAGAGAAAAGTCTCTA-AGTTTSTGGTGTACCAAATCATC
                                                                                                                                                                                                                                176 GCAAGGACCCAGCAGGAAGCACCAGCCACTGGCCGACCTCCCGACCCAGGAACCTGA
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                                                                                                                                                                                                                                                                                                               TCAGCAGTACTGGCAGAACCAGAAATGCCGCTGGAAGCACGTCAAACTGCTCTTTGAGAT
                                                                                                                                                                                       GGGCACTTAGACACACAGTGGCCTGAGCT-CCAACTCCAGCATGACCACGCGGGAGCT
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                                                               TCAGCAGTACTGGCAGAACCAGAAATGCCGCTGGAAGCACGTCAAACTGCTCTTTGAGAT
                                                                                                                                               AGGCACCTGCCCCCACACAGTGGAATAAAATAGAAACTCCAGGAGGATGACCACGCGGGGGAGCT
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Pred. No. 1.4e-84;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             drug; side effect; cancer; central nervous system; cardiovascular; qastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.
This invention describes a novel method for determining the degree of methylation of a particular cytosine in a mctif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic
                                                                                                                                                                                                                       Determining the degree of cytosine methylation in genomic DNA, for diagnosis and prognosis, comprises selective hybridization amplicons from chemically treated DNA \, -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oligonucleotide for detecting cytosine merhylation SEQ ID NO 4651
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                                                                                                                                                              Claim 12; 56pp + Sequence Listing; 56pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, cytosine methylation, 5' (pd.3', uracil,
                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-371829/40
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ABQ18061

ABQ18061 standard; DNA; 570 BP

12-JUL-2002

(first entry)

Oligonucleotide for detecting cytosine methylation SEQ ID NO 4652

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Similarity 76.3%;
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Pred No 1 4e-56;
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05-SEP-2000; 2000DE-1044543.
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                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 570 BP; 216 A; 202 C; 62 G; 90 T, 0 other;
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TOCCTOCOGOGOGOGOGASTACCCOCOGOGOGOCOTOCTOCTOCTOCOGOGOGTGCTGCCCCCTG
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                                                             CGCCGCTCCCGGGAGTTCCTGGACTTCCTCACGCGGCCGGAGCCTGCGCGAGGCTTTCCGCC
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                                   CHICAGETECTIANAATTECTIANAETTECTEAEGEGAEEGAAACTACGEGAAACTTTEGAE
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                                                                                     ABQ18058 standard; DNA; 570
Oligonucleotide for detecting cytosine methylation SEQ ID
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RESULT 8
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This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The meth

(i) for diagnosis and/or prognosis of side effects of

method

Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA $\,$ -

Claim 12; 56pp + Sequence Listing; 56pp; German

Olek

Piepenbrock C,

Berlin ζ,

Guetig

WPI; 2002-371829/40.

01-SEP-2000; 2000DE-1043826. 05-SEP-2000; 2000DE-1044543.

(EPIG-) EPIGENOMICS AG

01-SEP-2001; 2001WO-EP10074

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RESULT 9
ARQ18096
1D ARQ180
AC ARQ180
AC ARQ180
XX ARQ180
XX Oligon
XX Oligon
XX Oligon
XX Human;
KW drug;
KW gantro
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                                                                                           Human; cytosine methylation; 5'-CpG 3'; uracil, cytosine; diagnosis, drug; side effect; cancer; central nervous system; cardiovascular; qustrointestinal; respiratory system, single nucleotide polymorphism
                                                                                                                                                                                                                              Oligonucleotide for detecting cytosine methylation SEQ ID
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   Homo sapiens.
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This invention describes a novel method for determining the degree of CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a CC genomic sample of DNA. The sample is treated chemically to convert CC genomic sample of DNA. The sample is treated chemically to convert CC not convert of the genomic cytosine (C) but not methylated C, to uracil, then part of the genomic CC The amplicon is hybridised to two classes, each with at least one CC and the degree of hybridised to two classes is determined from the amplicon of classes is determined from the CC and the degree of hybridisation to both classes is determined from the CC classes of oligomers, the degree of methylation is calculated. The method is used. (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders CC therapeutic drugs and of a wide range of diseases, e.g. cancer disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's), and (ii) for differentiation of cell or tissue
                                                                                        types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously. ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-SEP-2000; 2000DE-1043826.
05-SEP-2000; 2000DE-1044543.
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                                             the disclosure of the invention.
                                                                 method for determining the degree of cytosine methylation described in
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단 밁 Бb Ş Ş B Ş 밁 Ş Ş Ş Query Match Best Local Matches 430; 583 450 463 403 343 CO-000CTATTCC05ACTTCC05AAACTCCA5AAA3CACTGCT5AAAAACTTCTGAAAAACACAC 643 CAGGAGAAAATTCACCGGCCACTGCCCTFGGGCCGCCGTCCCCGTCCCTGTCCCTTGTGCCGCCGCCTGCCTTG 390 523 TGTGAGCGTCGGCGCCCTGCAGGAGTACCTGGGCTGCTCTACGCCATCCGTTGCTTG ATOGAAGACGTGGAGTTTCCCAGGAAGCACCTGACTGGGAACTTCGCTGAGGAGAEATC 462 TAGGAGAAGTTTATCGTTTATTGTTTTTGCGGTCGTCGTTTCGGTTTTGTGCGTCGTGTTTG CGGCGTTATTTCGATTTCGCGAAGTTTTAGAAAGCGTTGTTGAAGACGTTTAGAGGAGGAC 511 ATCGAAGACGTGGAGTTTTTTAGGAAGTATTTGATTGGGAAATTTCGTTGAGGAGALGATT Similarity Conservative 36.4%, 0; Mismatches 139; Indels Score 346.6, DB 2 Pred. No. 3.3e-55; DB 24, Length 570 0; Gaps 702 271 391

Sequence 570 BP; 230 A; 197 C, 62 G, 81 T, 0 other;

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                                                                                                                                                                                                                                                           example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (1) by expressing inactive proteins or to supplement the patients own production of (1). Additionally, (1) polynucleotides may be used to produce the secreted (1), by inserting the nucleic acids into a host cell and culturing the cell to express the protein (1) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic related diseases, especially cancers and cancer metastases of haematopoietic derived cells. AAK64703
                                                                                                                                                                                                                                                                                                                                                                                                     amino acid sequences given in AAM92170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and merastasis -
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                                                                                                                                                                                      Sequence 588 BP; 140 A; 166 C; 167 G; 105 T; 10 other;
                                                                                                                                                                                                                                  to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 6849; 3071pp + Sequence Listing; English.
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                                                                                         1 ATGUCAAGTOCAGAGCAOOCTIVAGAGGCCCTIGGCTGGCATGGGACCCATAACCCAGTGCACG 60
ATGGCAAGTCCAGAGCACCCTGGGAGCCCTGGCATGGGACCCATAACCCAGTGCACG 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001-483426/52.
                                                                                                                           303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAM8900B
                                                                                                                                                                                                                  sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Parash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; 2000US 0249264,
; 2000US 0249265,
; 2000US-0249297,
; 2000US 0249299,
; 2000US-0249300,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US 0249216.

2000US-0249217.

2000US-0249218.

2000US 0249244.

2000US 0249244.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               220AHS.0256160
2000HS-0250391
2000HS-02510391
2000US-0251988
2000US-0251988
2000US-0251868
2000US-0251868
                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001US-0259678.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0251869.
2000US-0251989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0249211.
0249212.
0249213.
0249214.
                                                                                                                                        29.8%;
95.6%;
                                                                                                                          8; Mismatches
                                                                                                                                        Score 283, DB 22,
Pred. No. 1.8e-43;
                                                                                                                                                       DB 22,
                                                                                                                          Indels
                                                                                                                                                       Length 588,
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Gaps

63

sequences have activities such as: cytostatic; hepatotropic; vulnerary,

antipsoriatic, antiparkinsonian, nootropic; neuroprotective;

```
02-APR-1999;
05-APR-1999;
30-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antiviral, antibacterial, antifungal, antirheumatic, antithyroid; antianaemic, gene therapy, cancer, proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease, diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage, cartilage damage; antiinflammatory disease; coagulation; bone damage, cartilage damage; antiinflammatory disease; coagulation;
AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human CRFX open reading frames 1 to 3161. The GRFX
                                                                                                                                                                 Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-MAR-2000; 2000WO US08621.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypotensive; dermatological; immunosuppressive; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAC77276
                                                                                                       Claim 5;
                                                                                                                                                                                                                                                                                                       P-PSDB; AAB43067.
                                                                                                                                                                                                                                                                                                                                                                                                Shimkets RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human ORFX ORF2831 polymucleotide sequence SEQ ID NO:5661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08 FEB 2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               thrombosis; contraceptive; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Clib V - )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WICCAGAYIGGGAGIIT 488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAGCAGTACTGGCAGAACCAGAAATGCCGCTGGAAGCACGTCAAACTGCTCTTTGAGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CUPAGEN COPP
                                                                                                   Page 4838; 5507pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard, cDNA; 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000008-0540763
                                                                                                                                                                                                                                                                                                                                                                                                    Leach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0127636
99US-0127728
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RESULT 12
AAL45648
ID AAL45
XX AAL45
XX AAL45
XX Human
XX Human
XX Unide
FH Key
FH Key
FH CDS
FT CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antibacterial; antiviral; antifungal; antitheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an OREX-associated disorder. The
                                                                                                                                                                                                                                                                                                                       Human; cancer cell growth inhibitor; cancer; cytostatic; gene;
                                                                                                                                                                                                                                                                                                                                                                 Human cancer cell growth inhibitor related cDNA SEQ ID NO: 4.
                                                                                                                                                                                                                                                                                                                                                                                                            11-JUN-2002
(SHAN-) SHANGHAI CITY INST ONCOLOGY
                                        18-MAY-2000; 2000CN-0115744.
                                                                             18-MAY-2000;
                                                                                                                     05-DEC-2001.
                                                                                                                                                        CN1324819-A.
                                                                                                                                                                                                                                                                                            Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAL45648;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAL45648 standard; cDNA; 2064 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 578 BP; 149 A; 173 C; 169 G, 87 T, 0 other,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acids can be used to express ORFX proteins in gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  osteopathic; anticonvulsant; antiarthritic; immunosuppressant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 GCAAGTECAGAGCACCCTGGGAGGCCTGGGTGCATGGGACCCATAACCCAGTGCACGGCA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CACTTAGACACACAGTGGCCTGAGCTCCAACTCCAGCATGACCACGCGGGAGCTTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCAGCTCGCATCGAGGAGAAAAAGTCTCTAAGTTTGTGATG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCAGCTCGCATCGAGGAGAGAAAAGTCTCTAAGTTTGTGGTG 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CASTACTGACAGAACCAGAAATSCCGCTGGAAGCACGTCAAACTGCTCTTTGAGATCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGGACCCAGCAGGAAGCACCAGCCACTGGCCGCACCTCCCGCACCCAGGACCTGACGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCAAGTCCAGAGCACCCTGTGTGAGCCCTGTG-TGCATGGTACCCCATAACCCAGTGCACGGCA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGTACTGGCAGAACCAGAAATGCCGCTGGAAGCAGGTCAAACTGCTCTTTGAGATCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CACTTAGACACACACAGTOGCCTGAGCTCCAACTCCAGCATGACCACGCGGGAGCTTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             280;
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                                                                             2000CN-0115744.
                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                               Location/Qualifiers 317..871
                                                                                                                                                                                                           /*tag=
                                                                                                                                                                                             /product= "cancer cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29.2%;
                                                                                                                                                                                                           Q)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 268.4; DB 2
Pred. No. 8.6e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                           growth inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 21; Length 578;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                         related protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Gaps
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AAL45649
ID AAL4
XX
AC AAL4
XX
DT 11-J
XX
DE Huma

AAL45649; 11-JUN-2002

(first entry)

Human cancer cell growth inhibitor related DNA SEQ ID

RESULT 13

AAL45649 standard; DNA; 2064 BP

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention provides the protein and coding sequences of a number of human proteins capable of acting as cancer cell growth inhibitors. These can be used to inhibit cancer. The present sequence is a coding sequence described in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2064 BP; 459 A; 606 C, 597 G, 402 T, 0 other,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human protein, and the polynucleotide that encodes it, useful for inhibiting cancer cell growth \ \ \text{-}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gu J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 13-14(Disclosure); 31pp; Chinese.
   736
                                                                                                                                                                                                                                                                                                      616
                                                                                                                                                                                                                                                                                                                                                                                699
                                                                                                                                                                                                                                                                                                                                                                                                                                                       556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              642
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ()
()
                                                                      819 GGTCCGCCTGGCCTACGCGCTGGGCAAGGAC 849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        316 AATGGCTGCCATCTCCTTCCCCCGTAAGCGGGTGCGCCGGAATTTTACTGCAGAGACCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       196 GCTCTACACCCTCACCGTGATCGGCCCAGGACCGCCAGATTGCCCAGGCCAGGCCAGATCTC
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides the protein and coding sequences of a number of human proteins capable of acting as cancer cell growth inhibitors. These can be used to inhibit cancer. The present sequence is a coding sequence described in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2064 BP; 459 A; 606 C; 597 G; 402 T, 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human protein, and the polynucleotide that encodes it, useful for inhibiting cancer cell \text{growth} -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lung disorder, nose disorder; lung cancer; gene therapy; cytostatic; anti allergic; anti asthmatic; anti inflammatory; olfactory;
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AASIBICI AASIB764 represent genomic sequences encoding for novel human respiratory antigens.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                          6888
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Barash SC, Ruben SM;

WPI; 2001-483426/52

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis

Disclosure; SEQ ID NO 42060; 3071pp + Sequence Listing; English

AAKS4951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome to that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) compared to the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to produce the secreted (I), by inserting the culturing the cell to express the concers and cancer metastases of haematopoietic acids and cancer metastases of haematopoietic antigen genomic concers and cancer metastases of haematopoietic antigen genomic concers from the present invention. AAK54942 to AAK54950 and AAM82169 represent invention.

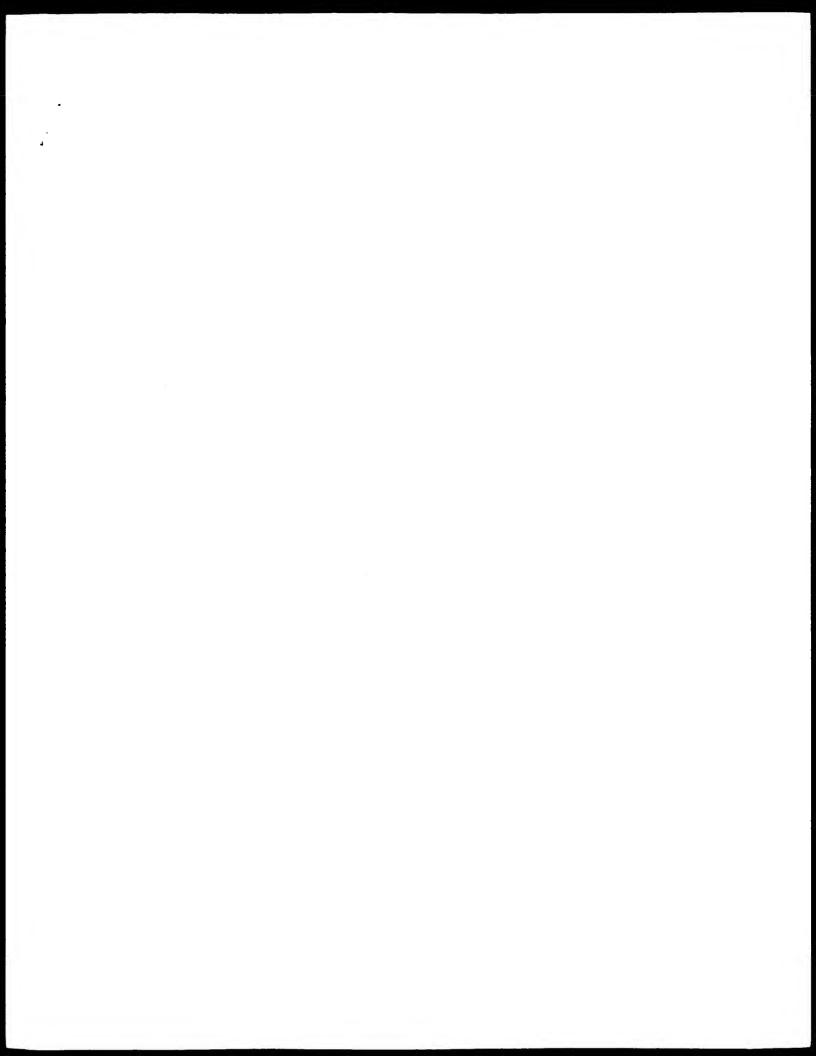
Sequence 23580 BP; 5938 A; 5961 C; 5927 G; 5754 T; 0 other,

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Query Match
Best Local 9
                            Matches 306; Conservative
Similarity
                                     14.3%;
                        Score 135.8; DB 22; Length Pred. No. 2.9e-16; 0; Mismatches 262; Indels
                                                 Length 23580;
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Scarch completed. April 20, 2003, 15.57:11 Job time: 975 secs



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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Sequence 57. Appl	Sequence 7925, Ap	Sequence 5, Appli	Sequence 3356, Ap	Sequence 5, Appl	Sequence 7, Appli	Sequence 1, Appl	Sequence 1, Appli		Sequence 28, Appl	Sequence 1, Appli	Sequence 115, App	Sequence 115, App	Sequence 3350,	Sequence 4009	Sequence 1, Appli	Sequence 260,	Sequence 990, App	Sequence 1, Appli	Description

ALIGNMENTS

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US-09-816-697-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:

APPLICANT: LOTENZ, M., et al.

TITLE OF INVENTION: A NOVEL P-SELECTIN GLYCOPROTEIN LIGAND (PSGL-1)

TITLE OF INVENTION: BINDING PROTEIN AND USES THEREFOR

FILE REFERENCE: GFN-5380

CURRENT APPLICATION NUMBER: US/09/816,697

CURRENT FILING DATE: 2001-03-23

PPIOR APPLICATION NUMBER: 60/192,104

PRIOR FILING DATE: 2000-03-24

NUMBER OF SEQ ID NOS: 4

NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 951
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
181 CAGCAGTACTGGCAGAAACCAGGAAATGCCGGCTGGAAAGCACGTCAAACTGCTCTTTGAGATC
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                                                                                                                                                                              GGGCACTTAGACACACACAGTGGCCTGAGCTCCAACTCCAGCATGACCACGACGCAGCGCGCGAGCTT
                                                                                                                                                       GCAAGGACCCAGCAGGAAGCACCAGCCACTOGCCCCGACCTCCCGCACCCAGGACCTGAC 120
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                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 990
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Mat ches
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                                                     Query Match
                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/764,860 CUPRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC008
                                                                                                                                                                                                                                                                      Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1198
                                                                                                                                 TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                          LENGTH: 23580
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SEC ID NO 260
LENGTH: 561
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Patent No. US20020168711A1
GENEPAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Mucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ32
CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT FILING DATE. 2001-01-17
Prior ATTIONALY.
    Matches 235,
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Best Local
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OTHER INFORMATION:
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CURRENT FILING DATE: 2001-05-17
PPIOP APPLICATION NUMBER: CA 2,106,241
PRIOR FILING DATE: 2000-05-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Bech-Hansen, Torben
TITLE OF INVENTION: GPI-Anchored Small Leucine-Pich Proteoglycan Gene NYX
FILE REFERENCE: 45499-2
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SOFTWARE: PatentIn version 3 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS: Bech-Hansen NT et al.
TITLE: Mutations in NYX, encoding the leucine-rich proteoglycan nyctalopin,
TITLE: cause X-linked complete congenital stationary night blindness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAGES: 319-323
DATE: 2000-11-01
DATABASE ACCESSION NUMBER: GenBank / AF254868
DATABASE ENTRY DATE: 2000-12 23
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SEQ ID NO 4009
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                                                                                                                                                                                                                                                         Query Match
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TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITEA.011A
CUPPENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE. 2001 03-21
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PRIOR FILING DATE: 2000-10-23
PRIOR AFFLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE. 2000-03-21
PRIOR APPLICATION NUMBER: 69/206,848
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PRIOR APPLICATION NUMBER: 69/207,727
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PRIOR APPLICATION NUMBER: 69/207,727
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Zyskind, Judith W.
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                                                                                                                                                                                                              APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
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PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-05 14
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Scherf, Uwe
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                                                                                                                                      ; Sequence 115, Application US/03874923 ; Patent No. US20020081320A1
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LENGTH: 7065
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                                                                                                                   GENERAL INFORMATION:
                  APPLICANT:
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                                                        APPLICANT: Reed, Steven G. APPLICANT: Campos-Neto, A APPLICANT: Webb, John R.
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APPLICANT: Brannon, Mark
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
TITLE OF INVENTION THERAPY AND BRAGHOGIS OF LEISHMANI
FILE REFERENCE: 210121.420C9
CURRENT APPLICATION NUMBER: US/09/991,496
CUPPERT FILING DATE: 2001-11-20
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    APPLICANT:
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Local Similarity 45.2%,
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Bhatia, Ajay
Coler, Rhea
                Dillon, Davin C. Skeiky, Yasir A.
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Bhatia, Ajay
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US-09-976-059-1
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; LENGTH: 7065
; TYPE: DNA
; OPGANISM: Leishmania major and chagasi
US-09-874-923-115
                                                                                                                                                               SEQ ID NO 1
LENGTH: 88
TYPE: DNA
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APPLICANT: Farnet, Chris
APPLICANT: Zazopoulos, Emmanuel
APPLICANT: Staffa, Alfredo
TITLE OF INVENTION: Genes and Proteins for Riosynthesis of Pamoplanin
FILE REFERENCE: 3019-PCT
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TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
TITLE OF INVENTION THERAPY AND DIAGNOSIS OF LEISHMANIASIS
FILE REFERENCE: 210121.420C8
CURRENT APPLICATION NUMBER: US/09/874,923
CURRENT FILIMG DATE: 2001-06-04
NUMBER OF SEQ ID NOS: 122
                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/976,059
CURRENT FILING DATE: 2001-10-15
NUMBER OF SEQ ID NOS: 34
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NAME/KEY: misc_feature
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LOCATION: (65826)...(66530)
CTHER INFORMATION: ORF 15; p
NAME/KEY: misc_feature
LOCATION: (66546)...(67370)
CTHER INFORMATION: ORF 16; p
NAME/KEY: misc_feature
LOCATION: (67364)...(70059)
CTHER INFORMATION: ORF 17; p
NAME/KEY: misc_feature
LOCATION: (70059)...(70662)
OTHER INFORMATION: OFF 18; p
NAME/KEY: misc_feature
LOCATION: (70059)...(71906)
CTHER INFORMATION: OFF 18; p
                                            NAME/KEY: misc feature LOCATION: (75424). (74213)
OTHER INFORMATION: ORF 22; ning feature LOCATION: (75535)...(76464)
OTHER INFORMATION: ORF 23; p
                                                                                                                                                                                   NAME/KEY: misc feature
LOCATION: (74216)..(73563)
OTHER INFORMATION: OFF 21;
                                                                                                                                                                                                                                                        NAME/KEY: misc feature
LOCATION: (73439)..(71964)
OTHER INFORMATION OFF 20;
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LOCATION: (15880)..(19035)
OTHER INFORMATION: OPF 12;
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LOCATION: (15591)..(15863)
OTHER INFCRMATION ORF 11;
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LOCATION: (6665)..(5814)
OTHER INFORMATION: ORF 4; negative
NAME/KEY: misc_feature
LOCATION: (78110)..(76449)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc feature
LOCATION: (39713)..(65800)
OTHER INFORMATION: OPF 14;
NAME/KEY: misc_feature
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LOCATION: (19032)..(39713)
CTHER INFORMATION ORF 13;
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LOCATION: (13617)..(12802)
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                                                                                                                                                                                                                                                                                                                             LOCATION: (70659)..(71906)
OTHER INFORMATION: ORF 19;
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LOCATION: (15203)..(13614)
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LOCATION: (4038)..(504)
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LOCATION: (3118)..(4032)
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OTHER INFORMATION: ORF 1; positive strandedness
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US 08 957-425-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Swquence 28, Application US/08957425 Publication No. US20030069401A1 GENERAL INFORMATION APPLICANT: OPPERMANN, HERMANN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 136; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hest
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41459 GTGGCCGACGCCTCTCCGÄÖGČTGĞĞTĞĞCĞÇÇ 41493
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LOCATION: (87494)..(88420)
OTHER INFORMATION: ORF 33; positive strandedness; N-terminus only
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (87372)..(86803)
OTHEP INFORMATION: ORF 32; positive strandedness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: (8555) (86845)
OTHER INFORMATION: OPF 11; positive strandedness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: (84481)..(85548)
OTHER INFORMATION: OPF 10; positive strandedness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: (82587)..(84446)
OTHER INFORMATION: OPF 29; positive strandedness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INCATION: (H2446) ... (H2062)
OTHER INFORMATION: OFF 28; negative strandedness
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LOCATION: (81909)..(81682)
OTHER INFORMATION: OPF 27; negative strandedness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: OFF 26; negative strandedness
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LOCATION: (79864) . (78107)
OTHEP INFOPMATION: OFF 25; negative strandedness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (H2346) ..(B26
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LOCATION: (81624), (79)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           781 GAGGGCCATCGCTACTATGCGCCTCTGCTGGACGC 815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          661 CACTROCCCTGLGGANNANTRICCNASTORTISTGRANDSTRATGCTASTORGASTASTORGASTC 720
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                                                                                                                                                                                                                                                 TITLE OF INVENTION: OSTEOGENIC DEVICES NUMBER OF SEQUENCES: 33
                                                                                                                                                                                                     CORRESPONDENCE ADDRESS.
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Similarity 49.5%;
                                                                                   CITY: BOSTON
                                                                                                                          ADDRESSEE: TESTA, HIRWITZ & THIBEAULT STREET: 53 STATE STREET
COUNTRY: U.S.A.
                                       STATE: MASSACHUSETTS
                                                                                                                                                                                                                                                                                                                                                                       KUBERASAMPATH, TI
RUEGER, DAVID C.
                                                                                                                                                                                                                                                                                                                                    PANG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           OZKAYNAK, ENGIN
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Best Local Similarity 48.8%; Pred. No. 0.00034; Matches 141; Conservative 9: Minmatches
                                                                                       08-957-425-28
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                                                                                                       /product: "hOP2-PP"
/note= "hOP2 (cDNA)"
SEQUENCE DESCRIPTION: SEQ ID NO: 28:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION
TELEPHONE. 617/248-7000
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                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                             FEATURE:
                                                                                                                                               OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN" /product: "hOP2-PP"
                                                                                                                                                                                      NAME/KEY:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Poloaso #1 C, Version #1 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 232,630
FILING DATE. 15-AUG 1988
APPLICATION NUMBER: US 179,460
FILING DATE. C8-AFP 1989
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                                                                                                                                                                                                                                                TISSUE TYPE: HIPPOCAMPUS
                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 617/248-7100
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CURPENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: 09/214,808
PRIOR FILING DATE: 1999-06 22
NUMBER OF SEQ ID NOS: 1
SCFTWAPE: Patentin Ver. 2.1
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APPLICANT: Broughton, William John
TITLE OF INVENTION: Genomic Sequence of Phizobium Sp. NGR 234 Symbiotic
TITLE OF INVENTION: Plasmid
FILE PEFFERNCE: CAPPO068
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APPLICANT: Freiberg, Chris
APPLICANT: Perret, Xavier |
APPLICANT: Broughton, Will
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APPLICANT: Zhao, L.
APPLICANT: Zhao, L.
APPLICANT: Zhao, L.
TITLE OF INVENTION: DNA encoding methymycin and pikromycin
FILE REFERNCE: 600.438US1
CURRENT APPLICATION NUMBER: US/09/861,289
CURRENT FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: 09/105,537
PRIOR FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE. FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 15872
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SEQ ID NO 1
LENGTH: 15872
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CURRENT APPLICATION NUMBER: US/03/550,846
CURRENT FILING DATE: 2001-05-18
PPIOR APPLICATION NUMBER: 09/105.537
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                                                                                                                                                                                                                                                                                                           Matches 170; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 133,
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Best Local Similarity 49.1%;
                                                                                                                                                                                                                                                                                                                                           Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Pompejus, Markus
APPLICANT: Suelberger, Harald
APPLICANT: Joeffken, Hans Wolfgang
                                                                                                                                                                                                                                                                                                                                                                                                                                   10 076 157 7
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SOFTWARE: WordPerfect v. 6.1
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TITLE OF INVENTION: Genes of purine biosynthesis from Ashbya Gossypii and the use the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Jimenez, Alberto;
APPLICANT: Garcia, Maria Ang
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TYPE: DNA

    534 ООНОСЛЕТАСССИВЗЕСЕСТВЗАН ПРИТЕСТВОННЕТОГОСТВОЛИТЕТОГО ПРИМЕНАСЛАСЛЯ В 53

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 09/155,421
PRIOR FILING DATE: 1998-09-29
PRIOR APPLICATION NUMBER: PCTINZ97/00040
PRIOR FILING DATE: 1997-03-27
PRIOR APPLICATION NUMBER: NZ 286284
PRIOR FILING DATE: 1996-03-29
NUMBER OF SEQ ID NOS: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lyttle, David J
APPLICANT: University of Otago
TITLE OF INVENTION: Parapoxvirus vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/796,679 CURRENT FILING DATE: 2001-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Robinson, Anthony J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 23607 MRB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SCFTWARE.
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ORGANISM. Orf virus strain NZ-2
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Search completed: April 20, 2003, 20:19:49 Job time : 664 secs

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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Maximum DB seg length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		% Ouery				
No	Score	Match		DB	ID	Description
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14	52.2		884	C1	.08-901-2	
15	'n		884	w	09-219-391-	11, App
16	N		72	_	07-841-646-2	28, App
17	2		72	ب	-07-901-703-	10, App
18			U	_	-08-147-023-2	28, App
19	Ļ)		72		-08 206-864-	3, Appl
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21	i)		72	١	-08-480-528A-	7, Appl
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25	13		72	_	08-643-563A	20, App
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20	Sequence 20, App	Sequence 5, Appl	Sequence 20, App	Sequence 7, Appl		Sequence 20, App	ក •	•	0.0		28,	Sequence 28, App	Sequence 7, Appl	Sequence 20, App	Sequence 5, Appl	Sequence 20, App	COMPANY OF A MARKET

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                                                                                                                                                                US-08-642-255-50
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                                                                    Query Match 6.0%; Score 56.6; DB 1; Length 756; Best Local Similarity 46.3%, Fred. No. 0.002, Matches 202; Conservative 0; Mismatches 254; Indels 3; Gaps
                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (415) 494-8700
TELEFAX: (415) 494-8771
TELEX: 910 277299 FHT UR
INFORMATION FOR SEQ ID NO: 50:
                                                                                                                                                                              TOPOLOGY: lin
MOLECULE TYPE:
DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                  NAME: ROWLAND, Bertram I.

REGISTRATION NUMBER: 20,015

REFERENCE/DOCKET NUMBER: A55556-3/BIR

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE FLEHP, HOHBACH, TEST, ALBRITTON & HERBERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: CAPPELIO, Joseph
APPLICANT: FERRARI, Franco A.
TITLE OF INVENTION: Protein Polymers
TITLE OF INVENTION: Protein Polymers
NUMBER OF SEQUENCES: 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER. US/0 FILING DATE: CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                      LENGTH: 756 base pairs
TYPE: nucleic acid
STRANDEDNESS, double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
398 AGGAGATCGAAGACGTGGAGTTTOCCAGGAAGCACTGACTGGGAACTTCGCTGAGGAGA 457
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                                                                                                                                                                                  other nucleic acid
/desc = "synthetic"
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RESULT 2
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                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO-
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: THOMAS G. PLANT 1501
STREET: LILLY CORPORATE CENTER
                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOO'KET NIMBER X-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-2459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: February
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Kuhstoss, Stuart A. APPLICANT: Rosteck, Paul R., Jr. APPLICANT: Sutton, Kimberly L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
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                                                                         MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTE: ING. COMPUTER: ING. COMPUTER: ING. COMPUTER: MS-10.0
OPERATING SYSTEM MS-10.0
OPERATING SYSTEM MS-10.0
OPERATING SYSTEM MS-10.0
OPERATING SYSTEM
OPERATION DATA:
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NAME/KET: CDS
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APPLICANT:
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                                                                                                                  ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                          OPERATING SYSTEM: Macintosh 7.0 SOFTWARE: Microsoft Word 5.1 CURRENT APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                             CORPESPONDENCE ADDRESS.
                                                                                                                                                                                                                                                                           APPLICANT: Posteck, Paul R., Jr.
TITLE OF INVENTION: PLATENOLIDE SYNTHASE GENE
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                             APPLICATION NUMBER: US/08/804,198 FILING DATE:
                                                                                                           COMPUTER:
                                                                                                                                                                                    STATE:
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Local Similarity 47 8%;
                CLASSIFICATION:
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Kuhstoss, Stuart A.
Rao, Nagaraja P
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                                                                                                                      Floppy disk
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                                                                                                                                                                                                                 Sequence 1, Application US/08209747
Patent No. 5733771
GENERAL INFORMATION:
APPLICANT: Lewis, Randolph V.
APPLICANT: Colgin, Mark
TITLE OF INVENTION: cDNAs Encoding Minor Ampullate Spider
TITLE OF INVENTION: Silk Proteins
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PEGISTRATION NUMBEP: 36,470
PETERENCE/DOCKET NUMBER: P9:
TELECOMMUNICATION INFOEMATION:
                                                                                                                                                    NUMBER OF SEQUENCES: 5
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ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
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350..14002
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; NAME/KEY: CDS; LOCATION: 183..2675; COTHER INFORMATION: /product= "N. clavipes () OTHER INFORMATION: ampullate silk protein" US-08-209-747-1
                                                                                                                                                                          ; Sequence 1, Application US/08458298 ; Patent No. 5756677
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Best Local Similarity
                                                                                                                                                       GENERAL INFORMATION:
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                APPLICANT: Lewis, Randolph V.
APPLICANT: Colgin, Mark
TITLE OF INVENTION: CDNAS Encoding
TITLE OF INVENTION: Silk Proteins
NUMBER OF SEQUENCES: 56
COPPRESPONDENCE ADDPESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 22040-3487
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FOR PC-DOS/MS-DOS
COFFFATING SYSTEM: PC-DOS/MS-DOS
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LENGTH: 2793 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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TELEPHONE: 703-205-8000
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                               2162 GGATACGSTGCCGSÄGSÄGSAGCTGCTGCAGCTGCTGGAGCAGCAGSAG 1207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  771 GCAGGCCCGGGAGGGCCATCGCTACTATGCGCTCTGCTGGAGGCCATGGTCCGCCTGGC 830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         711 CCGCGACCTCGACCGCCCGGCGAGGGCCTTCGCGGCGGGAGAGAGGGGCCCTGCAGCGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Murphy Jr., Gerald M. PEGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1447-104P
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ADDRESSEE: Birch, Stewart, Kolasch & Birch
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                                                                                   cDNAs Encoding Minor Ampullate Spider
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Sequence 5, Application US/C868C506C Parent No. 6008013 (GENERAL INFORMATION: APPLICANT: ReyNolds, Paul R.
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APPLICANT: Reynolds, Paul R.
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INFORMATION FOR SEQ ID NO. 1.
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
1.ENGTH: 2793-2034
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: 20040-3487
ZIP: 22040-3487
COMPUTER READABLE FORM:
TOTAL TYPE: Floppy disk
                                                                                                                                                  2162 GHATACCHTCHCHHACHTAGAGCTCHCTGCAGCTGCTGGAGCAGCAGCAG
                                                                                                                                                                                                                           2102 CCACGAGCTCGAGCCCGCTGGCAGSTGCTTGAAGCAGCTTGAAGCTTATACGTGSTSTCAAGGT 2163
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REFERENCE/DOCKET NUMBER. 144
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-225 8000
TELEPHONE: 703-225 8000
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/209,747
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ORGANISM: Nephila clavipes
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                                                                                                                                                                                                                                                                                                    2042 GOTGGTGTA-KIATA TABARIS GOTTA STABITTA Ó GOTA GA PETE CTUSTUS TORAS GOGGES EL 101
                                                                                                                                                                                       831 CTACGCGCTGGGGAAGGACTTCGTGACTCTGCAGGAGAGGCTGGAG 876
                                                                                                                                                                                                                                                                                                                                                                                                                771 GCAGGCCCGGGAGGGCCATCCCTACTATGCGCCTTCTGCTGGACGCCATGGTCGCCTGGC 830
                                                                                                                                                                                                                                                                                                                                       Local Similarity
hes 142; Conserv
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LOCATION: 183..2675
OTHER INFORMATION: /product= "N. clavipes r
OTHER INFORMATION: ampullate silk protein"
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CITY: Falls Church
STATE: Virginia
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DEDNESS. double
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SYSTEM: PC-DOS/MS-DOS
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; SEQ ID NO 8
; LENGTH: 1347
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LENGTH: 954
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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OTPRENT FILING DATE: 1996-07-08
EARLIER APPLICATION NUMBER: 60/021,672
EARLIEP FILING CATE: 1996-07-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Reynolds, Paul R.
TITLE OF INVENTION - CHONDROCYTE PROTEINS
FILE REFERENCE. 176/60091
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EARLIER FILING DATE: 1996-07-05
NUMBER OF SEQ ID NOS: 18
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CURRENT APPLICATION NUMBER: US/08/680,506C
CURRENT FILING DATE: 1996-07-08
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SOFTWARE. Patentin Ver. 1
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654 CACCGCCCACTGCCCTGCGGCCGCCGTCCCGGCCTyTyPCXCCTTTGCTGCTGTTGCCACCG 713
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Local Similarity 49.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 5.8%; Score 55.4; DB 3; Length 1347; Local Similarity 49.2%, Fred. No. 0.0038, es 146; Conservative 0; Mismatches 151; Indels 0
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Patent No. 6008013
GENERAL INFORMATION:
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
SOFTWAPE: PatentIn Ver.
SEQ ID NO 4
LENGTH: 2233
TYPE: DNA
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CURPENT APPLICATION NUMBER: US/09/690,506C
CURRENT FILING DATE: 1996-07-08
EARLIEF APPLICATION NUMBER: 60/021,672
EARLIER FILING DATE: 1996-07-05
                                                                                                                                                                 CUPPENT APPLICATION NUMBER: 12/03/680,5060
CURRENT FILING DATE: 1996-07-08
EARLIER PRPLICATION NUMBER: 60/021,672
EARLIER FILING DATE: 1996-07-05
NUMBER OF SEQ ID NOS: 18
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TITLE OF INVENTION: CHONDROCYTE PROTEINS
FILE REFERENCE: 176/60091
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TITLE OF INVENTION: CHONDROCYTE PROTEINS
FILE REFERENCE: 176/60091
CURRENT APPLICATION NUMBER: US/08/680,506C
CURRENT FILING DATE. 1996-07-08
EARLIER APPLICATION NUMBER 60/021,672
EARLIER FILING DATE. 1996-07-05
NUMBER OF SEQ ID NOS: 18
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SEQ ID NO 2
LENGTH: 5027
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Matches 146; Conservative
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APPLICANT: FERRARI, Franco A.
TITLE OF INVENTION: High Molecular Weight Collagen-Like
TITLE OF INVENTION: Protein Polymers
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                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: San Francisco
SOFTWARE:
                                                                                                                                                                        MEDIUM TYPE:
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VENTION: POLYMUCLEOTIDE VACCINE FORMULA AGAINST POPOINE
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PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FLEHR, HOHRACH, TEST, ALBRITTON & HERBERT
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                                                                                                                                                                  Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 5.6%;
Best Local Similarity 48.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE. (415) 494-8701
TELEPAX: (415) 494-8771
TELEX. 910 277299 FHT UR
INFORMATION FOR SEQ ID NO: 46
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       414 CGGTCCGGCAGG 425
                                    854 TGACTCTGCAGG 865
                                                                                                                                                    9
                                                                                                                                                                                                                        614 TGGAGCTGCTGCTGCGCGTGCTGCCGCTGTAGAAAAAACTTTACCGCCAATTACCTTGCCTTGCGG-673
                                                                                                                                                                                                                                                                                                                                                                                 117 TJJACCJJJCTJJTCCACCGGTGCCGANAČĆTGŠČAŠIČCCĞČAŠJTVAJJCCTGCACC 176
                                                                                                                                                                                                                                                                                                                                                                                                 354 เพิ่ยสามากอย่างคุณต่าที่อีกคลับอย่ายอย่ากคลับขอย่ากใหญ่จียต่าก็คลับอย่ากคลับคลับอย่ากคลับอย่างสังการตัว 413
                                                                                          794 ACTATGCG=CTCTGGTTGGACGCCATGGTCGGTCGGTTGGCCTACGGTGGGGTGTGGGAGAGACTTCCG 853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: ROWLAND, Bertram I REGISTRATION NUMBER. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 432 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                  ACCOSTROCTCOSSAUTTOCASSIÓLOCASSTSCUETTESALICISETTESTICÁTICACIDOS 853
                                                                                                                                                                                        AGGITTTTGGGGGCGGAGAGAGAGGTCTTGTAGCGCCTGCAGGCCCGGGGAGGCCCAG
                                                                                                                                                                                                                                                                                                     GÓCTOGTICANCOSOSTACTICASIANCITISCASIACIOS CON AGUTACIONO TARACTIGO (233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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RESULT 13
$196516-7
$196516-7
$PATENT NO. 5196516

APPLICANT: SCHREURS, CHRISTA S, METTENLEITEP, THOMAS C.
$SIMON, APPLY J.LUKAS, NOEMI, RIZHA, HANNS J.

TITLE OF INVENTION. PSEUDORABIES VIRUS VACCINE

NUMBER OF SEQUENCES: 8
CURRELT APPLICATION DATA:
APPLICATION NUMBER: US/07/383,833

FILLING DATE: 21-JUL-1989

$SEQ ID NO.7.
LENGTH: 4897

5196516-7

Query Match
Best Local Similarity 46.9%; Pred No 0.016;
Matches 165; Conservative 0; Mismatches 187; Indels 0;
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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11, Application US/08901200A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: OPPERMANN, HERMANN
APPLICANT: OZKAYNAK, ENGIN
APPLICANT: KUBERASAMPATH, THAN
APPLICANT: KUBGER, DAVID C.
                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (508) 435-6951 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: RUEGER, DAVID C. APPLICANT: PANG, ROY H.L. APPLICANT: COHEN, CHARLES M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2419 TÜACCACĞĞĞÜTCBBORRÂĞTTTĞÖĞĞĞGĞTĞĞAĞTTĞAĞĞTAĞĞACÇAÇAT 2490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: MEYERS, THOMAS C. REGISTRATION NUMBER: 36, REFERENCE/DOCKET NUMBER:
LOCATION: 1..884

COTHER INFORMATION: /note= "hOP-2 genomic sequence"
                                                                                      NAME/KEY: misc_feature LOCATION: 1..884
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/901,200A FILING DATE: 28-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE:
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                                                                                                                                                                                                                                                                                  STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
             FILING DATE: 28-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: MEYERS, THOMAS C.
REGISTRATION NUMBER: 36,989
REFERENCE/DOCKET NUMBER: CPP-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/901,200
                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: OP3-INDUCED MORPHOGENESIS NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    735 CTGGACCTGTACCACGCCATGGCCGGCGACGACGACGAGGACGGCGCGC 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           592 ССССОССАСТАСССОСОСОСОСТОЗАЭСТОСТЭСТВОЕВОЗГОСТВОЕВОВОЛЬНЫЙ 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  532 CGGGAGTTCCTGGACTTCCTCACGCGGGGGAAGTTGGGGGAGGGTTTTGGGCTGCCTGGGG 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 884
OTHER INFORMATION.
OTHER INFORMATION:
                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: exon LOCATION: 1..8
                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                              FILING DATE
                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                       CITY: HOPKINTON
                                                                                                                                                                                                                                                                                                                                                                                          STREET:
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TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                        E: PATENT ADMINISTRATOR, OPEATIVE BIOMOGROULES 45 SOUTH STREET
                                                                                                                                                                                                                                                                                                                                       USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RUEGER, DAVID C. PANG, ROY H.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OZKAYNAK, ENGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KUBERASAMPATH,
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(508) 435-9001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.5%;
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                                                                                                                                                                                             US/09/219,391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 52.2; DB 2;
Pred. No. 0.016;
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Search completed: April 20, 2003, 17:03:16
Job time : 290 secs
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INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 884 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                          Ouery Match 5.5%; Score 52.2; DB 3; Length 884; Hest Local Similarity 48.8%; Pred. No. 0.016; Matches 141; Conservative 0; Mismatches 148; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        09 219-391-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: exon
LOCATION: 1..837
OTHER INFORMATION: /note= "EXON ONE"
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: 1.884
OTHER INFORMATION: /note= "hOP=2 genomic sequence"
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic) FEATURE:
                                                                                                                                                                                                                                    592 GCCGGCCAGTACCCGCGGCGCCCTCCTGAAG TO TOTOGCGGTGCTGCTGCCGCTTGCAGGAGAAG 651
                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/REY: misc_feature
ILOCATION: 884
OTHER INFORMATION: /note= "A GAP OCCURS BETWEEN
OTHER INFORMATION: POSTIONS 884 IN THIS SEQUENCE AND POSITION 1 IN SEQ ID NO 14"
                                                                                                                                                                                                                                                                                                                                                           0; Gaps
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Title:
Perfect score:
                                                                              Database :
                                                                                                                Post-processing: Minimum March o%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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PIR_73:*
1: pir1.*
2: pir2.*
3: pir3:*
4: pir4:*
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1650
1 MASPEHPGSPGCMGPITQCT
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                                                                                                                                                                                                                                                                                                                                                                                     PPPTPPGITLKELTVREYLH 316
                                                                                                                                                                                                                                                   283224
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
	117	7.1	952	2	E84534	hypothetical prote
2	116	7.0	1010	N	10	tical stru
w	111	6.7	473	ıs	4.	hrcid alph
4	111		1104	Ν	97	to MDM
ر ت	111	6.7	2477	Н	JCHA	n alpha ch
6	102.5		1127	C1	S47445	rotein -
7	102		1030	c s	3261	trin alpha ch
8	101		1325	:0	479	ical pr
9	99.5		705	IJ	36	splice
10	99		475	N	A27671	alpi
11	99		2472	t J	A35715	lpha ch
12	98	5.9	459	Ν	T31608	hypothetical prote
13	97.5		420	L1	869	hypothetical prote
14	97		4684	2	940	plectin [imported]
15	96		441	2	8331	conserved hypothet
16	96		4574	N	0252	
17	95.5		373	2	8254	pon
18	95.5	5.8	398	t)	875202	prot
19	۷. دره		780	٠,	4093	Ω
20	95		943	ы	8293	ease
21	94.5	٠	1082	t J	8198	tical prot
22	5 80		578	C 1	T21345	prot
23	93		401	N	3904	l phox
24	93		475	N	2767	alph
25	93	5.6	1366	N	59	
26	92.5		\vdash	N	0553	probable serine/th
27	92		295	t s	4251	e
63			0	,		n Ia - bov
20				N	3041	

A/Cross references. EMBL.AL109957, FIDN.CAB53076.1; GSFDB.GN00068, SFDB.SFCC16A11.04

ALIGNMENTS

DD 606 IQLDKYLQDLLCIANVAEQHEVWUFLSAASKNYSFG 641 RESULT 2
159 RALQFYLGLLYAIRCVRRSREFLDFLTRPELREAFG
554 DVENKTWFVKRRYSNFERLHRQLKBIPNYNUQLPPKFIFSSSTEDAFVHRRC
Db 503 HNDWYISDWKSQSIVLHKEGGHCLKLKEFFEEIEDVEFFPRHIJGNFAKEMIJFPP-153
Query Match 7.1%; Score 117; DB 2; Length 952; Best Local Similarity 26.3%; Pred. No. 0.25; Matches 41; Conservative 25; Mismatches 70; Indels 20; Gaps 5; Qy 42 HLDTHSGLSSNSSMTTRELQQYWQNQKÇPWFHVKLLFEIASAPIEEPKVSKFVVYQIIVI 101
A;Status: preliminary A;Molecule type: DNA A;Residues: 1-952 <sto> A;Cross:references. GB.AE002093; HID.g5306243, FIDN.AAD41976.1, GSFDB.GN00139 C;Genetics: A;Gene: At2g15900 A;Map position: 2</sto>
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MJID:20083487; FMID:10617197 A;Accession: E84534
R;Lin, X; Kaul, S.; Pounsley, S.D.; Shea, T.P.; Benito, M.I; Town, C.D.; Fujii, C.Y. M; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999
RESULT 1 E84534 hypothetical protein At2g15900 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02.Feb.2001 #sequence_revision 02.Feb.2001 #text_change 02 Feb.2001 C;Accession: R84534
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C;Species: Gallus gallus (chicken)
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A;Map position: 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-473 <BIR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Remarkable homology among the internal repeats of erythroid and nonerythroid sp
A;Reference number: I50420; MUID:85298223, PMID:3862389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Birkenmeier, C.S.; Bodine, D.M.; Pepasky, E.A., Helfman, D.M., Hughes, S.H., Rurker, Proc. Natl. Acad. Sci. U.S.A. 82, 5671-5675, 1985
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related to MDM1 protein [imported] - Neurospora crassa
                                T49735
                                                           RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross references: GB:M11953; NID:g212696; PIDN:AAA49074.1, PID:g212697
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                                                                                                                                                                                                      282 KDFVTLQERLEE 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    263 KKNNHHVENTTAKMKGLKGKVSDLEKANAQRKAKLDE.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            143 PAIGGVLDTGKKLSDOWTIGKEEIGEKLAPFVDHWKELKQLAAARGQRLEESLEYQQFVA 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 PGPDGHLDTHSGLSSNSSMTTRELQQYWQNQKQRWKHVKLLFEIASARIEER-KVSKFV 94
                                                                                                                                                                                                                                                                                                                                                                      ADVVESWIGEKENSIKTDDYGPDLSSVQTLLTKQETFDAGLQAFQQEGIANITALKDQLL
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                                                                                                                                                                                                                                                        NAKHIOSKAIEVPHASLMKPWNQLLANSAAPKKLLEAQEHERKVECLFLTFAKKASAFN 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KTEREEIEDVEEPRKHLTGNEA--EEMICEPPRALQEYIGLIYAIRCVPRSPEFIDELTP 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44;
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                                                                                                                                                                                                                                                                                                                 --HRDLDRPAEAFAAGERALQR--LQAREGHRYYAPLLDAMVRLAYALG 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 7%; Score 111; DR 2; Length 473
21.2%; Pred. No. 0.32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44; Mismatches 134; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35; Mismatches
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Fred No ก 32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .. NSAFLQFNWK 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                      369
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A;Note: residues 1880-2359 are shown between residues 1399 and 1400 in Fig. 2 C;Suporfamily: spectrin alpha chain, calmodulin repeat homology; 3H3 homology; spectrin/cC;Keywords, actin binding, calcium binding, cytoskeletton; duplication; EF hand; heterodin F;43:147/Domain. spectrin/dystrophin repeat homology <SP1> F;148-253/Domain: spectrin/dystrophin repeat homology <SP2> F;254-359/Domain. spectrin/dystrophin repeat homology <SP3>
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C;Species: Neurospora crassa
C;Date: 02 Jun 2000 #sequence_revision 02 7:n 2000 #*ext_change 02 Jun 2000
                                                               F;677-782/Domain: spectrin/dystrophin repeat F;783-88/Domain: spectrin/dystrophin repeat F;889-973/Domain: spectrin/dystrophin repeat F;974-1021/Domain: SH3 homology <SH3>
                                                                                                                                                                                             F;360-465/Domain: spectrin/dystrophin repeat homology <SP4>
F;466-571/Domain: spectrin/dystrophin repeat homology <SP5>
F;572-676/Domain: spectrin/dystrophin repeat homology <SP6>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Molecule type. mRNA
A;Residues: 1-2477 <WA2>
A;Cross-references: EMBL:X13701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Title: Primary structure of the brain alpha-spectrin. A, Reference number. A31866; MJID:89093238, FMID:2910879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Cross-references. GB.X14519
P;Wassming, V.M.; Saraste, M.;
J. Cell Biol. 108, 79-93, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Molecule type. mRNA
A; Residues: 1-2477 < WAS>
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A;Contents. erratum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 01-Aug 1997 ()Accession. A3:122, A3:1866, A2:2733, S9:2425, S0:190 R;Wasenius, V.M.; Saraste, M.; Salven, F.; Eraemaa, M., Holm, L., Lehto, V.I.J. Cell Biol. 108, 1177-1178, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     H;Alternate names: calspectin alpha chain, fodiin alpha chain C;Species: Gallus gallus (chicken)
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A;Residues: 1-1104 <SCH>
A;Residues: 1-1104 <SCH>
A;Cross:references. EMBL.AL356192, GSPDB GROATI6, NGSP BC4B19 70
A;Experimental source: BAC clone B24B19; strain OR74A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R,Schulte, U., Aign, V., Hoheisel, J., Brandt, F., F. submitted to the Protein Sequence Database, May 2000 A,Reference number: 225022
A,Recession: T49735
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,1090 1231/Domain: spectrin/dystrophin repeat homology #status atypical <SP10>
,1232 1337/Domain: spectrin/dystrophin repeat homology <SP11>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  162 QEYLGLLYAIRCVPRSPEFLDFLTP 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        771
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   731 SKASLQRETRRKELQRQQYVTQESDNSLYGRSTIKIKNIHVGREFDGKEFAMYATEVLRN 790
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       M.; Salven, F.; Eraemaa, M., Holm, L.,
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                                                                                              homology
                                                                                                                                                                 homology <SP7>
                                                                                                                                     homology
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                                                                                                  #status atypical <SP9>
                                                                                                                                     <SP8>
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F;1338-1443/Domain: spectrin/dystrophin repeat hon F;1444-1549/Domain: spectrin/dystrophin repeat hon F;1550-1661/Domain: spectrin/dystrophin repeat hon F;1562-1767/Domain: spectrin/dystrophin repeat hon F;1768-1873/Domain: spectrin/dystrophin repeat hon F;1768-1873/Domain: spectrin/dystrophin repeat hor F;1874-1979/Domain: spectrin/dystrophin repeat hor F;1890-2086/Domain: spectrin/dystrophin repeat hor F;2095-2200/Domain: spectrin/dystrophin repeat hor F;2095-2200/Domain: spectrin/dystrophin repeat hor F;2028-2350/Domain: calmodulin repeat homology <EEF;2371-2401/Domain: calmodulin repeat homology <EEF
A.Title: Nuclear and mitochondrial inheritance in yeast depends on novel cytoplasmic st A.Peference number: A42636; MUID:92332595; PMID:1378448
A;Recession: A42636
A;Rocession: A42636
A;Molecule type: DNA
A;Residues: 685-771, 'P', 773-898,'I', 900-1062,'K',1064-1080,'S',1082-1095,'R',1097-1127
A;Cross references: EMBL:X66371; NID:g3915; PIDN:CAA47014.1, PID:g3916
A;Note: sequence extracted from NCBI backbone (NCBIN.108433, NCBIF.108434)
R;Stirling, C.J.
R;Stirling, C.J.
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S47445
                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:Z49210; MIFS.YML104c
R;McConnell, S.J.; Yaffe, M.P.
J. Cell Biol. 118, 385-395, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                              A;Reference number: S53954
A;Accession: S53968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:X80835; NID:g530339; PID:g530340; MIPS:YML104c R;Skelton, J.; Churcher, C.M. submitted to the EMBL Data Library, May 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-676 < BAR >
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Saccharomyces cerevisiae
C;Date: 02-Dec-1994 #sequence_revision 06-Sep-1996 #text_change 21.Jul.2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MDM1 protein - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein 0 13: protein YM8339 15c; protein YML104c
C;Species: Saccharomyces cerevisiae
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A;Residues: 673-1127 <SKE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAKHIQSKAIEVRHASLMKRWNQLLANSAARKKKLLEAQEHFRKVEDLFLTFAKKASAFN 2109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADVVESWIGEKENSÜKTDDYGPDI.SSVQTLLTKQETFDAGLQAFQQEGIANITALKDQLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KKNNHHVENITAKMKGLKGKVSDLEKAAAQRKAKLDE------NSAFLQFNWK 1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAIQGVLDTGKKLSDDNTIGKEEIQQRLAQFVDHWKELKQLAAARGQRLEESLEYQQFVA 1882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PGPDGHLDTHSGLSSNSSMTTPFIQQYWQNQKCPWKHVKLLFEIASAPIEEP-KVSKFV- 94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -HPDIDPPAEAFAAGEPALOP--IQAPEGHPYYAPLIDAMVELAYALG 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 111;
Fred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --VYQIIVIQTGSFDNNKAVLERRYSDFAKLQKALL 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             homology <SP12>
homology <SP13>
homology <SP14>
homology <SP15>
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spectrin alpha chain, nonerythroid - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-May-1990 #sequence_revision 21 May-1990 #text_change 29-Sep-1999
C;Accession: A32612
R;Hong, W; Doyle, D.
T. Biol. Chem. 264, 12758-12764, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 1-1030 <HON>
A;Residues: 1-1030 <HON>
A;Cross-references: GB:Z44828, NID g273013, FIDM-AAA47770 1, FID:g203014
A;Cross-references: GB:Z44828, NID g273013, FIDM-AAA47770 1, FID:g203014
C;Superfamily: spectrin alpha chain; calmodulin repeat homology; SH3 homology; spectrin/0;Keywords: actin binding; cytoskeleton; EF hand
E;47-152/Domain: spectrin/dystrophin repeat homology <SP12>
E;799-904/Domain: spectrin/dystrophin repeat homology <SP19>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Biol. Chem. 264, 12758-12764, 1989
A;Title: Cloning and analysis of cDNA clones for rat kidney alpha-spectrin.
A;Reference number: A32612; MUID.89327227; FMID.2753883
A;Accession: A32612
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A;Cross-references.
A;Map position: 13L
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A;Accession: S51916
A;Molecule type: DNA
A;Residues: 874·1127 <STI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;913-1019/Domain: spectrin/dystrophin repeat homology <SP20>
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                              236 CHRDLDRPAEAFAAGERALQP-----
                                                                                                                                                                                                                        129
                                                                                                                                                                                                                                                                  587 NVEEEEAWINEKMTLVASEDYGDTLAAIOGLLKKHEAFETDFTVHKDRVNDVCTNGODLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      896 RFLTDP 901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182 DFLTRP 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42
                                                                                                                                                                                                                                                                                                                                                                                                          37 PGPDGHLDTHSGLSSNSSMTTRELQQYWQNQKCRWKHVKLLFEIASAPIEEP-KVSKFV- 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79 -EIASARIEEPKVSKFVVYQIIVI-----QTGSFDNNKAVLERRYSDFAKLQKALLKTF 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RDIMPQLQDL-FPSKVKMSLKYHVTKTLLYE---EPKQKLEYYLPELLSISEICEDNIFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FE---EIEDVEFFFK-----HUTGNFAEEMICEFFFALQFYLGLLYAIRCVFRSREFL 181
                                                                        ADVVESWIGEKENSÍKTOFÝGFÐÍSSVOTLÍTKÓÉTFÐÁGLÐÁFÐÐEGTÁNITÁÍKÐÐÍÍ.
                                                                                                                      PELREAF-----GCLRAGQYPRALELLLRVLPLQEKLTAHCPA-----AAVPALCAVLL
                                                                                                                                                                        KKNNHHEENISSKMKGINGKVSDLEKAAAQPKAKLDE------NSAFLQFNWK
                                                                                                                                                                                                                   KTERFEIEDVEFPRKHLTGNFA--SEMICERPRALOEYLGLLYAIRCVPRSPEFLDFLTR 186
                                                                                                                                                                                                                                                                                                                                                             PAIQGVLDTGKKLSDDNTIGQEBIĞĞRLAQFVEHWKELKQLAAARGQFLEESLEYQQFVA 586
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.2%; Score 102; DB
20.4%; Pred. No. 4.4;
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                                                                                                                                                                                                                                                                                                                  -----VYQIIVIQTGSFDNNKAVLERRYSDFAKLQKALL 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               46;
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Pred. No. 4.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches 132; Indels
-----IQAPEGHPYYAPLLDAMVPLAYA 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 1030;
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C;Species: Homo sapiens (man)
C;Date: 17-Aug-1990 #sequence revision 17-Aug-1990 #text_change 01-Dec C;Accession: A35363; B35363; A35805
R;Suedhof, T.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 8
T14790
A;Accession: B35363
A;Status: pinliminary
A;Molecule type: DNA
                                                                                                                                                                                        J. Biol. Chem. 265, 7849-7852, 1990
A;Title: The structure of the human synapsin I gene and protein
A;Reference number: A35363; MUID:90243651; PMID:2110562
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A;Molecule type: mRNA
A;Residues: 1 1325 <BLU>
A;Cross-references: EMBL,AL110273
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(;Date: 20-Sep-1999 #sequence revision 20-Sep-1999 #text_change 09 Jun 2000
(;Arrussion: T14790
                                                                                                             A; Molecule type: DNA
A; Residues: 1-705 < SUE>
                                                                                                                                                                 A; Accession: A35363
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C;Keywords: EF hand
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                                                                                A;Cross-references: GB:M58371; GB:J05431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1094 SWFENAEEDLTD 1105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1034 AAKHVQSKAIEAPHASLMKPWSQLLANSAAPKKKLLEAQSHFEKVEDLFLTFAKKASAFN 1093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  282 KDEVTLOFFLEE 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                974 ADVVESWIGEKENSLKTDNYGPDLSSVQTLLTKQETFDAGLQAFQQEGIANITALKDQLL 1033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   867 NVEREEAWINEKMTLVASEDYGDTLAAIQGLLKEHEAFETDFTVHKDRVNDVCTNGQDLI 926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             807 PAIQGVLDTGKKISDDNTIGKEEIQQRLAQFVEHWKELKQLAAARGQRLEESLEYQQFVA 866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  812 FNSWFENAEEDLTD 825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      280 LGKDFVTLQERLEE 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          754 AAKHIQ--SKAIEARHASLMKPWTQLLANSATPKKKLEAQSHFRKVEDLELTFAKKASA 811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  y Match 6.1%; Score 101; DB 2; Length 1325;
Local Similarity 20.8%, Pred No. 7 1;
Nes 65; Conservative 43; Mismatches 136; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37 PGPDGHLDTHSGLSSNSSMTTRELOOYWONOKCFWKHVKLLFEIASAPIEER-KVSKFV- 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PELREAF----GCLPAGQYPRALELLLRVLPLQEKLTAHCPA-----AAVPALCAVLL 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KKNNHHEENISSKMEGLNGKVSDLEKAAAQRKAKLDE....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----HPDI.DPPAEAFAAGERALQR--LQAREGHRYYAPILDAMVRLAYALG 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------VYQIIVIQTGSFDNNKAVLERRYSDFAKLQKALL 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .... NSAFLQFNWK 973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68;
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A;Molecule type: mRNA
A;Residues: 1-475 < LED:
A;Residue 1: PID: g205642
A;Residue 1: PID: g205642
A;Rote: the authors translated the codon GGC for residue 18 as Ser, GAG for residue 45 at er, AGA for residue 68 as Gln, CCG for residue 75 as Leu, and GAG for residue 76 as Ala c,Superfamily: spectrin alpha chain; calmodulin repeat homology, SH3 homology, spectrin/CCKeywords: actin binding; EF hand
C;Keywords: actin binding; EF hand
F;205 311/Domain: spectrin/dystrophin repeat homology < SP18 >
F;329 425/C:main: spectrin/3ystrophin repeat homology < SP19 >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Lero, T.L.; Fortugno-Erikson, D; Harton, D; Yang-Feng, TL; Francke, H; Harris, A; Mol. Cell. Biol. 8, 1-9, 1988
Mol. Cell. Biol. 8, 1-9, 1988
A;Title: Comparison of nonerythroid alpha spectrin genes reveals strict hemology among di
A;Reference number: A03097; MUID:88094373; PMID:3336352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             spectrin alpha chain, nonerythroid - rat (fragment)
c;Species: Rattus norvegicus (Norway rat)
C;Date. 19 May 1989 #sequence_revision 19 May-1989 #text_change 29-Sep-1999
C;Accession: A27671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references. GDB.119606, OMIM.313440
A;Map position: Xp11 23-Xp11.23
C;Keywords: actin binding; alternative splicing; phosphoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-125 < SAU >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Residues: 1 659, 'KASPAOAQF' <832>
A,Residues: 1 659, 'KASPAOAQF' <832>
A,Crooss-references: GB.M58378; GB:J05431
F;Sauerwald, A, Hicesche, C, Cochwald, F., Kilimann, M.W.
F;Sauerwald, A, Hicesche, C, Oschwald, F.,
J Biol Chem 265, 14932-14937, 1990
A;Title: The K'-flanking region of the synapsin I gene. A G+C-rich, TATA- and CAAT-less, A;Peference number: A35805; MNID:9036867; PMID:2118519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: GDB: SYN1
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                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           207 YAGIPSVNSLHSVYNFCDKP-WVFAQMVPLHKKLGTEE-----FPLID 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    224 AAAVPALCAVILICHPILIDPFAEAFAAGEFALGRIGAPEGHRYYAPILD 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          171 -----GVKVVRSLKP--DFVLIR---QHAFSMAKNGDY-RSL-----VIGLQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 IDEPHTDWAKYFKG--KKIHGEIDIKVEQAEFSDLNLVAHANGGFSVDMEVLRN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113 LERRYSDFAKLQKALLKTEPEE1 · · · · EDVEFPR ·
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Local Similarity 25.0%;
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1-4
94 V-----VYQIIVIQTGSFENNKAVLERKYSDFAKLQKA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32 PPPPGAHSPGATPGPGTATAERSSGVAPAASPAAPSPGSSGGGGFFSSLSNAVKQTT--- 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 PEHPG--SPGCM-GPITQCTARTQQEAPATGPULPHPGPUGHLUTHSGLSSNSSMTTREL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LGLLYAIRCVRRSREELDE-LTEPELPEAPGCLPAGGYPPALELLLPVLFLGEKLTAHCP 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QQYWQNQXQXWXHVXLLTEIASARIEERKVSKFVVYQIIVIQTGSFDNNKA-----V 112
                                                                         PECAICSVLDSGKKLIDDNTIGREBIGGRPEGEVEHWERLEGLAAARGGPLEESLEYCGE 105
                                                                                                                                                  PHPGPDGHLDTHSGLSSNSSMTTRELQQYWQNQKCPWKHVKLLFEIASAPIEEP-KVSKF 93
                                                                                                                                                                                                                            64,
                                                                                                                                                                                                                            Conservative 47, Mismatches 135,
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                                                                                                                                                                                                                                                           6.0%;
20.4%;
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                                                                                                                                                                                                                                                               Score 99; D
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                                                                                                                                                                                                                                                                                                 DB 2; Length 475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FHLTGNFAEEMICERRALQEY 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---VGGGSGGAGRGGAASRVLLV 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96;
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                                                                                                                                                                                                                            68;
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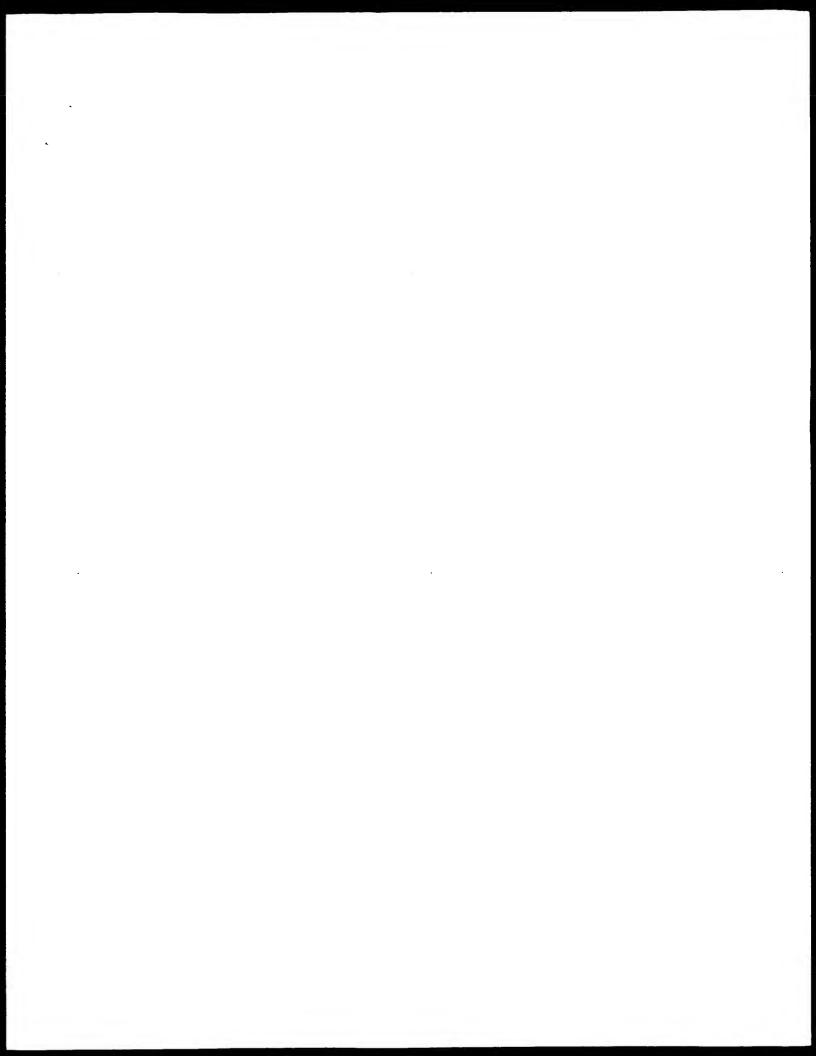
VANVEEEEAWINEKMTI, VASEDYGDTLAAIQGLLKKHEAFETDETVHKDEVNDVCTNOQD 165

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R;Mutha, S.; Langston, A.; Bonifas, J.M.; Epstein Jr., E.H.
J. Invest. Dermatol. 97, 383-388, 1991
A;Title: Biochemical identification of alpha-fodrin and protein 4.1 in human keratinocyt
A;Reference number: A61369; MMID:91341201, PMID:1875039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 1-2472 <MOO>
A;Cross references: GB.J05243; NID.g179135, PIDN:AAA51790.1; FID:g179106
R;McMahon, A P : Giebelhaus, D H; Champion, J E; Bailes, J.A; Lacey, S.;
Differentiation 34, 68-78, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N;Alternate names: alpha II spectrin; nonerythroid alpha-spectrin (Spectes: Homo sapiens (man) C;Daectes: Homo sapiens (man) C;Date: 05-Oct-1990 #sequence revision 05-Oct-1990 #text change 13-Aug-1990 C;Accession: A35715; A35580, T53382, A61369; G01810; S54877; S65683 R;Moon, R T; McMahon, A P
                                                                                          R;Lundberg, S.; Bjoerk, J.; Loefvenberg, L.; Backmann, L. submitted to the EMBL Data Library, May 1995
A;Description: Cloning and characterization of two putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Pesidues: 'P',1595-1510,'E',1612-1614,'P',1616-1624,'S',1626-1638,'P',1640,'E',1642-16
2-1813'P',1915 1820,'K',1822-1844,'V',1846-1850 <MUT>
A;Note. the sequence in Fig. 4 is inconsistent with the sequence in Fig. 3 at several pd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: cDNA cloning, sequencing and chromosome mapping of a non-erythroid spectrin, A;Peference number: A:8580; MUID:87277023; PMID:3038643
A;Accession: A28580
                                    A;Reference number: S54877
A;Accession: S54877
                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 811-1299, 'I', 1301-1529 <MOR>
                                                                                                                                                                                                                                                                                                                                                A;Reference number: G08473
A;Accession: G01810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A:Cross-references: GB:M24773; MID-q537330; PIDN-AAA52468.1; PID:q537331
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A; Residues: 676-1594, 'P' < PES>
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Biochem. Soc. Trans. 15, 804-807, 1987
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A;Status: preliminary
                                                                                                                                                                                                                                                                                                        A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, May 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                     R; Morrow,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: A61369
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A;Title: Generation of diversity in nonerythroid spectrins Multiple polypeptides are
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                                                                                                                                                                                                   Cross-references: EMBL:U26396; NID.g836668, PIDM:AAB60364.1, PID.g836669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     , J.S.
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                                                                                             calcium-binding
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hypothetical protein Y50E8A.d - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29 Oct.1999 #sequence_revision 29-0at-1999 #text_change 29-0at-1999
A;Experimental source: clone Y50E8A C;Genetics:
                                                                                                                                                                    submitted to the EMBL Data A; Reference number: Z21047 A; Accession: T31608
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T31608
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F:2264-2310/Domain: spectrin/dystrophin repeat homolo
F:213-2155/Domain: calmodulin repeat homology cEF1>
F:2166-2398/Domain: calmodulin repeat homology cEF2>
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C;Keywords; actin binding; EF hand
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: mRNA
A;Residues: 2059-2312,'F',2314-2346,'EF',2349-2433 <LUN>
A;Cross-references: EMBL:X86901
                                                A;Cross-references. EMBL:ALL17200, NID:e1549770; PIDN:CAR55047.1; CESP:Y50E8A.d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;677-782/Domain: spectrin/dystrophin repeat homology <SP7>F;974-1021/Domain: SH3 homology <SH3>
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A; Residues: 2320.2346, 'EF', 2349
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Eur. J. Biochem. 230, 658-665, 1995
                                                                                  A; Residues: 1-459 <WIL>
                                                                                                             A; Molecule type: DNA
                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                               R;Steward,
                                                                                                                                                                                                                                                                                       C;Accession:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1992 IGEKENSIKTDDYGRDISSVQTLLTKQETFDAGLQAFQQEGIANITALKDQLLAAKHVQS 2051
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1878 N---VEEEEAWINERMTLVASEDYGDTLAAIQGLLEEGHEAFETAFTVIKUKVNOVOTNGO 1934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2052 KAIEAPHASLMKFWCCII.ANSAAPKKKLLEAQSHFRKVEDLFLTFAKKASAFNSWFENAE 2111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             139 EFPRKHLTGNFAEEMICERPRALQEYLGLLYAIRCVPPSP-----EFLDFLTRPELREAF 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37 PGPDGHLDTHSGLSSNSSMTTRELQQYWQNQKCFWKHVKLLFEIASARIEER-KVSKFVV 95
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Pred. No. 22;
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R;Liu, C.G.; Maercker, C.; Castanon, M.J.; Hauptmann, R.; Wiche, G. Proc. Natl. Acad. Sci. N.S.A. 93, 4278-4283, 1996
A;Title: Human plectin: organization of the gene, sequence analysis, and chromosome loca A;Reference number. GC9404; MTTD-96216632, PMTD 8633065.
A;Accession: C59404
                                                                                                                                                                C;Sprcies: Homo sapiens (man)
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 19-Apr-2002
C;Accression: C59404; A59404
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C;Date: 11.Jun-1999 #sequence_revision 11-Jun-1999 #rext_change 13-Aug-1999
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A;Cross-references: EMBL-AL049989
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A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        173 CVRRSPEFI.DFI.TPPE--I.PEAFGCLPAGQYPPALELLLRVLPLQEKLTAHCPAAAVPAL 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      377 LAQKHPEHQDEFSREETTLREEF---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79 IETFITYRIITKTSRGEFDSSEFEVRRRYQDFLWLKGKLEEAHPTLIIPPLPE-----KF 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90 VSKEVVYQIIV-IQTGSEDNNKAVLERBYSDE-- AKLQKA----LLKTEREEIEDVEE 140
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28.5%; Pred No 3.4;
vative 26; Mismatches
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A;Molecule type: DNA
A;Residues: 1-4684 <STO>
A;Cross references: GB.CAA31196, HID:g1296662, FIDH.CAA91196.1
C;Superfamily: plectin; alpha-actinin actin-binding domain homology; ribosomal protein S;
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A;Peference number: ARC950; MUID:20437337, FMID:10984043
A;Accession: C83318
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P;Stover, C.K.; Fham, X.Q.; Erwin, A.L., Mizeguchi, S.D.; Warrener, P.; Hickey, M.J.; Bri adman, S.; Yuan, Y., Broly, L.; Coulter, S.R., Folger, F.F.; Far, A., Lathig, F.; Lim, Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   conserved hypothetical protein FA2613 [imported] - Fseudomonas acruginosa (strain FA01) C;Species: Pseudomonas acruginosa C;Spact: 15:Sep-2000 #sequence_revision 15 Sep-2000 #text_charge 31-Dec 2000
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A; Residues: 1-441 < STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Superfamily: Haemophilus influenzae conserved hypothetical protein H11590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: PA2613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      752 LESLHSFVAAATKELMWLNEKEEE 775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      270 LDAMVRLAYALGKDFVTLQERLEE 293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              635 APATQVAQVTLQSVQRRPELEDSTLRYLQDLLAMVEENQHPVDGAEWGVDLPSVEAQLGS 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             222 CPANAV ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         575 VERDLDKADSMIPLLFNDVQTLKDGRHÞQGSEQMYPÞVYPI.HEÞI.VAIÞTEYNI.ÞI.KAGVA 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180 FLDFLTRPE--LREAFG---CLRAGQYPRALELLLRVLPLQEKLTA-------H 221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             455 WSQFLEFEEMELPAKEADKNESKGIYQSLEGAVQAGQLKVPPGYHPLDVEKEWGELHVAI 514
                                                               128 VERSTRIFTGATTEMESFELNWALLSFAFVYVLKSLLEAALRFRVSKALMEDFRGSFFFU 187
                                                                                                                                                                                                                                                                                                                                                 / Match 5.8%; Score 96; DB 2; Length 441; Local Similarity 21.4%; Pred. No. 4.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IAIIJ.... 26
                                                                                                                                                                                       72 DAHFETISAVLSG----VKEIR@AVEVAK@HAAQYGRFTILFVDEVHRFNKSQQDAFLPY 127
                                                                                                                                                                                                                                                40 DGHLDTHSGLSSNSSMTTFELAQYWQNQK---CPWKHVKLLFEIASAPIEEPKVSKEVVY 96
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                                                                                                                                                                                                                                                                                                                      Conservative
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-LKTFREEIEDVEFPRKHLTGNFAEEMICERRR-----A 160
                                                                                                                                                                                                                                                                                                                   47; Mismatches 132; Indels 114;
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Muridae; Buteleostomi; Muridae; Murinae; Mus. Muridae; Murinae; Mus. Adachi J., Famiukuda S., Kondo S., Yamanaka I., Kasukawa T., Saito R., Lov S., Casavant T., Mushama Barsh G., P., de Bonaldo M.F., Am., Magner L., Washic T., Mr., Wagner L., Washic T., Mr., Wagner L., Washic T., Mr., Gariboldi M., J., Kamiya M., Lee N. H., ali J., Mombaers P., I., Sakamoto N., Storch KF., Whittaker C., Wilming L., Shibata Y., Storch KF., Whittaker C., Wilming L., Whittaker C., Wilming L., Shibata Y., Storch KF., Whittaker C., Wilming L., Whittaker C., Wilming L., Shibata Y., Storch KF., Whittaker C., Wilming L., Whittaker C., Washida P., Wh	Q9qxs1 mus musculu 29ry:2 deinecrocus P34531 caenorhabdi Q11102 caenorhabdi Q9hib2 thermoplasm 060749 homo sapien P74876 salmonella Q90640 gallus gall Q9w663 coturnix co P10826 homo sapien Q13596 homo sapien Q13596 homo sapien Q13596 homo sapien

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Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R., Jones M., Stavrides G., Almeida J.P., Babbage A K., Bagguley C L., Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M., Bearsley O.P., Bird C P., Plakey S E., Bridgeman A.M., Brown A.J., Buck D., Burrill W.D., Burler A P., Carder C., Carrer N.P., Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C M., Clark G., Corby N.E., Coulson A., Coville G.J., Deadman P., Dhami P.D., Dunn M.,
                                                                                                                                                                                                                                                                   MEDLINE_21638749; PubMed 11780052
                                                                                                                                                                                                                                                                                                                                                           Stavrides G.S., Huckle E.J., Deloukas P.; Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enkaryota, Metazoa,
Mammalia, Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sorting nexin 21.
SNX21 OP C200PF161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q969T3; Q9BR16;
I5-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00787; PX; 1.
SMART; SM00312; PX; 1.
PROSITE; PS50195; PX; 1.
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                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N A
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNXL HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transport; Protein transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001683; PX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241
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B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRGITIKELTVREYL 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AKLOKALIKTEREETEDVEEPPKHLTGNEAEEMICEPRPALOEYLGLIYATRCVPRSREF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QQYWQNQKCPWKHVKILFEIASARIEERKVSKFVVYQIIVIQTGSFDNNKAVLERRYSDF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ERPAEAFAVGERALRCLPTPENHPYYAPLLDAMVRLAYALGKDFAALQSFLDENQLPPPT 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DRPAEAFAAGERALQRLQAREGHRYYAPLLDAMVRLAYALGKDFVTLQERLEESQLRRPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LDFLTRPELBEAFGCLPAGQYPRALELLLRVLPLQEKLTAHCPAAAVPALCAVLLCHRDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QEHWQKEKSPWKHVPLLFETASARTEEEKKVSKFVMYQVVVTQTGSFDSDKAVVERRYSDF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LDFLTRPELREAFGCLRAGGYAPALELLGRALPLQEKLTAHCPSAAVPÄLCAALVCLRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                313 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata,
Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76.0%; Score 1253.5; DB 77.5%; Pred. No. 1.6e-96;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata, Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EBFCD04FA22707C3 CRC64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43; Indels
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RRA Grafham D.V., Griffiths C., Griffiths M.D., Gwilliam P., Hall P.E.,
RRA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RRA Hinckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RRA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
Lchvaslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RRA Kay M.P., Warrin S.L., McConnachie L.J., McLay K., McMurray A. A.,
RRA Milne S.A., Mistry D., Moore M.J.F., Mollikin J.C., Nickerson T.,
RRA Milme S.A., Mistry D., Moore M.J.F., Mollikin J.C., Nickerson T.,
RRA Milme S.A., Patel P., Pearce T.A.V., Peak A.I.,
RRA Milmore R.J.C.T., Prathalingam S.P., Phimb P.M., Pamsay H.,
RRA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen P., Sims S.,
RRA Swann P.M., Sycamore N., Taylor P., Tee L., Thomas D.M., Thorpe A.,
RRA Swann P.M., Sycamore N., Taylor P., Tee L., Thomas D.M., Thorpe A.,
RRA Milmend S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RRA Whitehead S.L., Whittaker P., Willey D.L., Williams S.A.,
RRA Whitehead S.L., Whittaker P., Willey D.L., Williams S.A.,
RRA Wilming J., Wray P.W., Hubbard T., Furbin P.M., Bentley D.R., Beck S.,
RRA Milmend M., Way P.W., Hubbard T., Furbin P.M., Bentley D.R., Beck S.,
RRA Milmend M., Way P.W., Hubbard T., Furbin P.M., Bentley D.R., Beck S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transport; Protein transport.
DOMAIN 129 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00515; TPR; 1. Pfam; PF00787; PX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, AL591562; CAC39140.1, -
EMBL; AL008726; CAC36011.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genew; HGNC.16154;
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InterPro; IPR001440; TPF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81 GPDGLPLGDGTSGENAERSPPPDGGW-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31 GPD-FP-----HPGPPGHTTTHSGLSSNSSMTTRELQDYWDNDKCRWKHVKLL 77
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SIMILAPITY BELONGS TO THE SOPTING HEXIN FAMILY.
VREYL 315
                                                                       LODESTHEITALETEWHANTER
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                                                                                                                                               LOARESHRYYAPILINAMVRIAYALGKIFVTLOERLEESQLERFTFRGIT
                                                                                                                                                                                                                      TGLYREALACMANAMQUQAQUSTES SEPRELLITIAGLAV HQELEPPSEAFA TEKADQL
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                                                               · LIFE_JEARL_ALGEAGLITTI i FGLEBLL
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Best Local
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Q9NRS6; Q9NRS5;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transport; Protein transport; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001683; PX.
Pfam; PF00787; PX; 1.
SMART; SM00312; PX; 1.
PROSITE; PS50195; PX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MIM; 605964;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genew; HGNC:14978; SNX15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      involved in protein trafficking.";

J. Biol Chem. 276:5074-5084(2001).

-!- FUNCTION MAY BE INVOLVED IN SEVERAL STAGES OF INTRACELLULAR TRAFFICKING. OVEREXPRESSION OF SNX15 DISRUPTS THE NORMAL TRAFFICKING OF PROTEINS FROM THE PLASMA MEMBBANE TO RECYCLING TRAFFICKING OF PROTEINS FROM THE PLASMA MEMBBANE TO RECYCLING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phillips S.A., Barr V.A., Haft D H., Taylor S I , Haft C P , "Identification and characterization of snx15, a novel sorting nexin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21265032; PubMed=11085978; Phillips S.A., Barr V.A., Haft D H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A
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                                                                          124
          246 AFAAGERALQRL---
                                                                                                                                          194
                                                                                                                                                                                                                                                                                                                                13
                                                                                                                                                                                                      73
                                                                                                                                                                                                                                                                                                                                                                                  78 FEIASARIEERKVSKFVVYQIIVIQTGSFDNNKAVLERRYSDFAKLQKALLKTFREEIED 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENDOSOMES OR THE TGN.
ALTERNATIVE PRODUCTS: 2 ISOFORMS: 1 (SHOWN HERE)
ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: WIDELY EXPRESSED.
SIMILARITY: BELONGS TO THE SORTING NEXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: CONTAINS 1 PX DOMAIN.
                                                                ---RGGEVTRPLEVSRDLHILPPPLIPT---PPPDDPRLSQLLPAERRGLEELEVFVDPP
                                                                                                                            GCLRAGQYPRALEII.--LEVLPLQEKLTAHCPAAAVPALCAVLLCHR----DLDRPAE-- 245
                                                                                                                                                                                            LEEFPAFPRAQVFGPFEASVIEERPKGAEDLLRFTVHIPALNNS----
                                                                                                                                                                                                                                                         VE----FPRKHLTGNFAEEMICEPPRALQEYLGLLYAIRCVERSREFLDFLTRPELREAF 193
                                                                                                                                                                                                                                                                                                                     YTVSDPRTHPKGYTEYKVTAOFISKKDPEDVKEVVVWKPYSDFPKLHGDLAYTHPNLFRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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---QAREGHRYYAPLLDAMVRLAYALGKDFVTLQERLEESQLRRP 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.5%; Score 123; DB 1; 24.9%; Pred. No. 0.0055;
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                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer entities requires a license agreement (See http://www.isb-sib.ch/annou or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                     Pfam; PF00787; PX; 1.
SMART; SM00312; FX; 1.
PROSITE; PS50195; PX; 1.
                                                                                                                                                                                                                                                                                                            EMBL; AF139461; AAD32668.1; -.
EMBL; AY044655; AAK98769.1; -.
EMBL; BC010886; AAH10886.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhang W., Wan T., Cao X.; "Hypothetical human protein Submitted (MAR-1999) to the
                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                          Transport; Protein transport.
DOMAIN 1 125
                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUN-2002 (Rel. 41,
15-JUN-2002 (Rel. 41,
15-JUN-2002 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SBBI31 as a new member
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNXO
                                                          139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: CONTAINS 1 PX DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FISSUE=Lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       L5-JUN-2002
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192 AFGC 195
                                                                                                                                                                                                                                                                                                 nterPro; IPR001683; PX.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        178 PSSPAQEALDLLFNCESTEEASGSPARGPLTEAELALFDPFSK--
                            57
                                                                                                               80 IASAPIEEPKVSK-FVVYQIIVIQTGSFDNNKAVLERRYSDFAKLQKALLKTFREEIEDV 138
                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           trafficking (By similarity).
SIMILAPITY: BELONGS TO THE SORTING NEXIN FAMILY.
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                         EIPSKHVR-NWVPKVLEQRRQGLETYLQAV-----ILENEELPKLFLDFLNVRHLPSLPK 110
                                                     EFPRKHLTGNFAEEMICERRRALQEYLGLLYAIRCVRRSRE----FLDFLT---RPELRE 191
                                                                                   IPSERYEESDLEPGYTVFKIEVLMNG----PKHFVEKPYSEFHALHKKIKKC----IKTP
                                                                                                                                                40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (JUL-2001)
                                                                                                                                                                                                         169 AA,
                                                                                                                                                Conservative
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                                                                                                                                             7.2%; Score 118; DB 1; 32 3%; Pred No. 0 006; ative 22; Mismatches 40
                                                                                                                                                                                                         19818 MW;
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Last annotation update)
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EMBL/GenBank/DDBJ databases
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Best Local Similarity
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                                                                                    SPCN CHICK P07751;
                                                                                                                      CHICK
                                   01-AUG-1988 (Rel. 08, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
16-0CT-2001 (Pel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
           Spectrin alpha chain, brain (Spectrin, (Fodrin alpha chain).
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "A novel member (SNX27) of the sorting nexin family."; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EnParyora; Motazca; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthoria; Primates; Catarrhini; Hominidae; Homo.
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ptam; PF00787; PX; 1
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InterPro; IPR000159; PA_domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hong W
                                                                                                                                                                                171 ESD 173
                                                                                                                                                                                                               186 RPE 188
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                                                                                                                                                                                                                                                                                                    RYKHV------EQNGEKFVVYNVYMA -----GRQLCSKRYREFAILHQNL-- 114
                                                                                                                                                                                                                                                                      TFREEIEDVEFPRKHLTG----NFAEEMICERRRALQEYLGLLYAIRCVRRSREFLDFLT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF00788; RA;
                                                                                                                                                                                                                                          -KREFANFTFPR--LPGKWPFSLSEQQLDARPRGLEEYLEFVCSIPVIGESDIMQEFLS 170
                                                                                                                                                                                                                                                                                                                                                                                                                              180
435 AA;
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                                                                                                     STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                               6.8%; Score 112 5; DE 28 5%; Pred No 0 055;
                                                                                                                                                                                                                                                                                                                                                                22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                           RA
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                                                                                                     2477
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                        non-erythroid alpha chain)
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                                                                                                                                                                                                                                                                                                                                                              37, Indels 29,
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NM AND MC DOMAINS ARE COMPOSED OF TYPICAL SPECTPIN 106 RESIDUES REPEATS (1-8 FOR NM AND 12-19 FOR NC) AND ARE HOMOLOGOUS TO EACH OTHER N, M, AND C DOMAINS ARE COMPOSED OF SEQUENCES THAT DO NOT FORM TYPICAL SPECTRIN REPEATS.
SIMILARITY: BELONGS TO THE SPECTRIN FAMILY.
SIMILARITY: CONTAINS 1 SH3 DOMAIN.

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MEDLINE-96067121, FubMed=7588621;
Trave G., Lacombe J.-P., Pfuhl M., Saraste M., Pastore A.;
"Molecular mechanism of the calcium-induced conformational change in
                                                                                                                                                                                                                                                                        -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the spectrin EF-hands.";
EMBO J. 14.4922-4931(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98022917; PubMed=9356261;
Pascual J., Fithl M., Walther D., Saraste M., Nilges M.;
"Solution structure of the spectrin repeat: a left-handed
antiparallel triple-helical coiled-coil.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Musacchio A., Noble M., Pauptit R., Wierenga R., Saraste M., "Crystal structure of a Src-homology 3 (SH3) domain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wasenius V.-M., Saraste M., Knowles J., Virtanen I., Lehto V.-P., "Sequencing of the chicken non-erythroid spectrin cDNA reveals an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1695-2153 FROM N.A.
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Lehto V.-P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRUCTURE BY NMP OF 2320-2403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRUCTURE BY NMR OF 1763-1872
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 359:851-855(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 965-1025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBO J. 4:1425-1430(1985).
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                                                                                                                                                                                                                                                                                                                             FUNCTION: MORPHOLOGICALLY, SPECTRIN-LIKE PROTEINS APPEAR TO RELATED TO SPECTRIN, SHOWING A FLEXIBLE POP-LIKE STRUCTURE. THEY CAN BIND ACTIVITY IN SEEM TO DIFFER IN THEIR CAMPODULIN-RINGING ACTIVITY. IN NOMERYTHEOID TISSUES, SPECTRINS, IN ASSOCIATION WITH SOME OTHER PROTEINS, MAY FLAY AN IMPOFTANT
                                                                                                                                                                  DOMAIN: SPECTRIN-LIKE PROTEINS HAVE FIVE DOMAINS
                                                                                                                                                                                                                                                                     ROLE IN MEMBRANE ORGANIZATION.
SUBUNIT: LIKE EPYTHPOCYTE SPECTFIN,
(5) <del>(4</del>)
                                                                                                                                                                                                                                         ARE CAPABLE TO FORM DIMERS WHICH CAN FURTHER ASSOCIATE
                                                                                                                                                                                                     TETRAMERS.
   C-TERMINAL DOMAIN (C)
                        MIDDLE DOMAIN (M), DOMAIN BETWEEN THE MIDDLE AND C-TERMINAL DOMAIN (MC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biol. 108:79-93(1989).
                                                                                               DOMAIN BETWEEN THE N-TERMINAL AND MIDDLE DOMAIN (NM)
                                                                                                                                  N-TERMINAL DOMAIN (N)
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                                                                                                                                                                                                                                                                     THE SPECTPIN-LIKE PROTEINS
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SMART; SM00054; EFh; 2.
SMART; SM00326; SH3; 1.
SMART; SM00150; SPEC; 20.
PPOSITE; PS00018; EF HAND; 2
PROSITE; PS50002; SH3; 1.
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                                                                       TURN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cytoskeleton; Membrane; Calmodulin binding; Actin-binding; Cappling protein; Calcium-binding; Repeat; SH3 domain; 3D-s DOMAIN 1 14 N-TERMINAL DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00036; efhand; 2.
Pfam; PF00435; spectrin; 23.
PRINTS; PR00452; SH3DOMAIN.
PrcDom; PD000012; EF-hand; 1.
PrcDom; PD000066; SH3; 1.
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EMBL; X14519; CAA32663.1;
EMBL; X02593; CAB51571.1;
EMBL; X02593; SJCHA
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1AJ3; 07-JUL-97.
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EF-HAND 2 (POTENTIAL)
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SEQUENCE
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16-CCT-2001 (Rel. 40,
15-JUN-2002 (Rel. 41,
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MDM1 OR YML104C OR YM8339.15C.
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                      This SWISS-PROT entry is copyright
                                                                                                                                                                                                                                                                                                             SEQUENCE OF 874-112/ FROM N.A Stirling C.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=92332595, PubMed-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Walsh S.V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                          "Nuclear and mitochondrial inheritance in yeast depends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 633-1127 FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Devlin K., Skelton J., Churcher C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomycetales;
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MDM1_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         129
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                                                                                      SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: TO S.POMBE SPCCIA11.04.
SIMILARITY: CONTAINS 1 PX DOMAIN.
SIMILARITY: CONTAINS 1 PXA DOMAIN.
CANTION: Pef 2 sequence differs from that shown due
                                                                  frameshift in position 638.
                                                                                                                                                                                                                                  inheritance.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION, AND SUBSELLULAR LOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AD4C876994E6AB39 CRC64,
                It is produced through
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Pfam; PFO0
Pfam; PFO0
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STRAIN-Wistar; TISSUE-Liver; Kalamaraki P., Gazzotti P.; "Kalamaraki P., Gazzotti P.; "Structural and functional characterization of the calmodulin calpain binding domains of rat liver alphaII spectrin."; Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                             Rattus norvegicus (Rat).
Eukaryora; Meraroa; Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Rodenria; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                          P16086; P70477; O88663;
01-APR-1990 (Rel. 14, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2007 (Rel. 41, Last annotation update)
Spectrin alpha chain, brain (Spectrin, non-erythroid alpha chain)
(Alpha-II spectrin) (Fodrin alpha chain).
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SGD;
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                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                           NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPCN RAT
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InterPro; IPR003114; PX_assoc.
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EMBL; X69210; CAA8911 1; ALT_INIT.
EMBL; X66371; CAA47014 1; ALT_FRAME.
EMBL; X667R1; CAA46664 1; -
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S0004572; MDM1.
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129380 MW, 70
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R InterPrc, lravell, R Refam; PF00018; SH3; 1.

R Pfam; PF00036; efhand; 2.

DR Pfam; PF00035; spectrin; 33.

DR SMART; SM00354, EFh. 2.

DR SMART; SM00150; SH3; 1.

DR ROSITE; PS00018; EF HAND; 2.

DR PROSITE; PS00018; EF HAND; 2.

DR PROSITE; PS00002; SH3; 1.

SP PROSITE; PS00002; SH3; 1.

SP PROSITE; PS00002; SH3; 1.

SP PROSITE; PS00002; SH3; 1.

Carring Protein; Calcium-binding; Repeat; SH3 domain.

SPECTRIN 1.

SPECTRIN 1.
   REPEAT
REPEAT
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REPEAT
REPEAT
                                                                                                       DOMAIN
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REPEAT
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EMBL; AF084186; AAC33127:1; -
EMBL; J04828, AAA40770:; -
ETR, A32612; A32612.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhou D , Ursitti J A , Porter N C , Pandall W P , Rluch R.J.; "Expressional cloning of alpha-fodrin from rat skeletal muscle."; Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
TISSUE=Skeletal muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (S or send an email to licensewisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/annonnce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS FROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Cloning and analysis of cDNA clones for rat kidney alpha-spectrin.";
J. Biol Chem 264 12759-12764 (1989)
--- FUNCTION: FORTH, WHICH SEEMS TO BE INVOLVED IN SECRETION,
INTERACTS WITH CALMODULIN IN A CALCIUM-DEPENDENT MANNER AND IS
THUS CANDIDATE FOR THE CALCIUM-DEPENDENT MOVEMENT OF THE
                        REPEAT
                                      REPEAT
                                                                                                                                          REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1292-2321 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IFR001452;
                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE SPECTRIN FAMILY.
SIMILARITY: CONTAINS 2 EF-HAND CALLUM-BINDING DOMAINS
SIMILARITY: CONTAINS 1 SH3 DOWAIN.
SIMILARITY CONTAINS 23 SPECTFIN PEPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOSKELETON AT THE MEMBRANE (By similarity). SUBUNIT: LIKE EPYTHROCYTE SPECTRIN, THE SPECTPIN-LIKE PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TETRAMERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ARE CAPABLE TO FORM DIMERS WHICH CAN FURTHER ASSOCIATE
                                                                                                                                                                                                                                                                                                                                                                                                                  £07751, 1AJ3
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  1062
1091
1208
1233
1233
1339
1445
1551
1658
1764
1764
 SH3
                                                                                                                                                                                                                                                                                                                                                                                                      EF-hand
                                                                                                                                                                              SPECTRIN 3.
SPECTRIN 4.
SPECTRIN 5.
SPECTRIN 6.
SPECTRIN 7.
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RESULT 9
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CA_BIND
CA_BIND
                                                                                                                                                                   Hanson B.J., Hong W.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: May be involved in several stages of intracellular trafficking (By similarity).
-!- SIMILARITY: BELONGS TO THE SORTING NEXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                            HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 193B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1878
EMBL; AF305779; AAG25676.1; HSSP; P14598; 1GD5.
                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                  the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer
                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                       Eukaryota; Metazca; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                  Sorting nexin 16
                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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16-0CT-2001
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                                                                                                                                                          SIMILARITY: CONTAINS 1 PX DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FNSWFENAEEDLTD 2116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LGKDFVTLQERLEE 293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NVEEEEAWINEKMTIVASEDYGDTLAAIQGLLKKHEAFETDFTVHKDRVNDVCTNGQDLI 1937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PAIQGVLDTGKKLSDDNTIGQEEIQQPLAQFVEHWKELKQLAAARGQRLEESLEYQQFVA 1877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PGPDGHLDTHSGLSSNSSMTTRELQQYWQNQKCRWKHVKLLFEIASARIEER-KVSKFV-
                                                                                                                                                                                                                                                                                                                                                                                                                              HUMAN
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Similarity 20.4%;
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2336
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SPECTRIN 23.

EF-HAND 1 (POTENTIAL).

EF HAND 2 (POTENTIAL).

D -> Y (IN REF. 1).

V -> L (IN REF. 1).

L -> AV (IN REF. 1).

KL -> NV (IN REF. 1).

KL -> NV (IN REF. 1).

OCICARNITGYT -> HADPGGEHUPSH (IN PEF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MW; 08DDF01A2871278A CRC64,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -- VYQIIVIQTGSFDNNKAVLERRYSDFAKLQKALL 128
                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                             343 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --NSAFLQFNWK 1984
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SPCN
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Best Local Similarity
Matches 41; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         O13813; Q16606, Q9FOVC, Q13186; Q170V-1997 (Rel. 35, Created)
O1-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Spectrin alpha chain, brain (Spectrin, non-erythroid alpha chain)
SPTAN1 OR SPTA2.
Homo sanian '''
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00787; PX; 1.
SMART; SM00312; PX; 1.
PROSITE; PS5C195; PX; 1
                                                                                      SEQUENCE OF 676-1595 FROM N.A.
MEDLINE=87277023; FubMed=3038643,
MCMahon A.P., Glebelhaus D.H., Champion J.E., Bailes J.A., Lacey S.,
MCMahon A.P., Mochman S.K., Moon R.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transport, Protein transport, Coiled coil.
DOMAIN 105 218 PX.
   McMahon A.P.,
                    ERRATUM
                                           "cDNA cloning, sequencing and chromosome mapping spectrin, human alpha-fodrin."; Differentiation 34:68-78(1987).
                                                                                                                                                                                                                 McMahon A.P., Moon R.T.;
                                                                                                                                                                                                                               MEDLINE=88083942; PubMed=3691949;
                                                                                                                                                                                                                                                                                         "Complete cDNA sequence of human alpha II fetal brain spectrin.";
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                      TISSUE=Fetal brain;
Cianci C.D., Morrow J.S.;
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                    the
                                                                                                                                                                                                                                                                                                                                                                                                            "Generation of diversity in nonerythroid spectrins. Multiple polypeptides are predicted by sequence analysis of cCNAs enumpassing
                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=90170948; PubMed=2307671;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa, Chordata; Craniata, Vertebrata, Eutelcostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                   alpha-fodrin."
                                                                                                                                                                                                                                                              SEQUENCE OF 676-1595 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       185
                                                                                                                                                                                                 "Structure and evolution of a non-erythroid spectrin, human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101 IQTGSFDNNKAVLEPRYSDFAKLQ---KALLKTFREEIEDVEFPRKHLTGNFAEEMICER 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     158 RRALQEYLGLLYAIRCVRRS---REFL 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78 TGTASSIEYSTRPRDTEEQNPETVNWEDRPSTPTILGYEV----MEER--AKFTVYKILV 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47 SGLSSNSSMTTRELQQYWQN-QKCRWKH
                                                                                                                                                                                                                                                                                                                                                                                    B: ~1
                                                                                                                                                                                                                                                                                                                                                                                  coding region of human nonerythroid alpha-spectrin."; sicl them 2ff 4407-4433(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QLGLQAFLQNLVAHKDIANCLAVREFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41;
                                                                                                                                                                                                                                                                                                                                                                                                                                               T., McMahon A P;
                                                                                                                                                                    Soc.
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                                                                                                                                                                    Trans. 15:804-807(1987)
Giebelhaus D.H., Champion J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     £.1%;
27.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COILED COIL (POTEMTIAL).
BBE772209BA46FF5 CRC64;
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(1)
   Bailes J.A.,
                                                                           of.
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(1
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Lacey S.,

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SMART; SM00054; EFh; 2.
SMART; SM000754; SH1; 1
SMART; SM000150; SPEC; 20.
PROSITE; PS00018; EF HAND; 1.
PROSITE; PS00002; SH3; 1.
CHICLE PSS WORLD SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Site-directed mutagenesis of alpha II spectrin at codon 1175 modulates its mu-calpain susceptibility.";
Biochemistry 36:57-65(1997).
               REPEAT
                                                            REPEAT
REPEAT
                                                                                                                                                                                                                                                             Pfam;
Pfam;
Pfam;
                                                                                                                                                                                                                                                                                                                                                                                EMBL; J05243; AAA51790.1; --
EMBL; U83867; AAB41498.1; --
EMBL; M24773; AAA52468 1; --
EMBL; M18627; AAA51702.1; --
EMBL; M18627; AAA61702.1; --
EMBL; U26396; AAB60364.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                        Cytoskeleton; Membrane, Calmodulin binding, Actin binding, Cappil, plotein, Calcium-binding, Repeat, SH3 domain, PolyREPEAT 10 42 SPECTRIN 1.
                                                                                                                                                                                                                        ProDom; PD000012; EF-hand; 1. ProDom; PD000066; SH3; 1.
                                                                                                                                                                                                                                               Pfam; PF00036; efhand; 4, Pfam; PF00435; spectrin; 32. PRINTS; PR00452; SH3DOMAIN.
                                                                                                                                                                                                                                                                                                                                      MIM; 182810
                                                                                                                                                                                                                                                                                                                                                Genew;
                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensewisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1: SIMILAPITY: RELONGS TO THE SPECTRIN FAMILY.
-1: SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS
-1: SIMILARITY: CONTAINS 23 SPECTRIN PEPEATS
-1: SIMILAPITY: CONTAINS 23 SPECTRIN PEPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Fetal brain;
MEDLINE=97146462; FubMed-8993318;
   DOMAIN
                                     REPEAT
                                                   REPEAT
                                                                                        REPEAT
                                                                                                  REPEAT
                                                                                                                                                                                                                                                                                                                                                              HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1073-1349 FROM N A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 811-1529 FROM N A , VARIANT ILE-1300, AND MUTAGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carritt B., Henchman S K , Moon R.T.;
                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THUS CANDIDATE THE MEMBRANE.
CYTOSKELETON AT THE MEMBRANE.
SUBUNIT: LIKE ERYTHPOCYTE SPECTPIN, THE SPECTRIN-LIKE PROTEINS
TO FORM DIMERS WHICH CAN FURTHER ASSOCIATE TO
                                                                                                                                                                                                                                                                                                                                        P07751; IAEY.
W; HGNC-11273; SPTAN1
                                                                                                                                                                                                                                                                                   PF00018; SH3;
                                                                                                                                                                                                                                                                                                                                                                         AF148808;
                                                                                                                                                                                                                                                                                              IPR002048; FF hand.
IPR001452; SH3.
IPP002017; Spectrin
                                                                                                                                                                                                                                                                                                                                                                         AAF26672.1;
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 676
782
888
955
1026
                                                            465
571
SPECTRIN
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NAS CON CONTRACTOR NAS CONTRACTOR NA
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Best Local &
Matches 69
                                                                                                                                         SANN HUMAN STANDARD; FRT; 2
Q95L93; Q9H5U0;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
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                                       Homo sapiens (Human).
Eukarycta, Metazoa, Cherdata, Craniata, Vertebrata, Eutel
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAIQGVLDTGKKLSDDNTIGKEEIQQRLAQFVEHWKELKQLAAARGQRLEESLEYQQFVA 1877
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A -> D (IN REF. 2).
DG > EF (IN REF. 2).
V (IN REF. 2).
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N -> K (IN REF. 2)
F -> S (IN REF. 2).
V -> I (IN REF. 2).
V -> I (IN REF. 2).
N -> R (IN REF. 3 AND 4)
N -> S (IN REF. 2).
IA -> FD (IN REF. 2).
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SPECTRIN 15.
SPECTRIN 16.
SPECTRIN 17.
SPECTRIN 19.
SPECTRIN 20.
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SPECTRIN
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T -> I.
                                                          Craniata, Vertebrata, Euteleustumi;
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                                                                                                                                                                         update)
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Best Local
                                                                                                                                                                                                                                                                                                                     SYNI HUMAN STANDARD; PPT; 705 AA. P17600; 075825; 01-AUG-1990 (Rel. 15, Created) 01-OCT-1996 (Rel. 34, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isogai T., Sugano S.;
"NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                              HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www isb-sib ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hong W.; "A new member (SNX23) of the sorting nexin family."; "A new member (SNX23) to the EMBL/GenBank/DDBJ databases.
               Sauerwald A , Hoesche C., Oschwald R., Kilimann M.W.; "The 5'-flanking region of the synapsin I gene. A G+C-rich, TATA- and CAAT-less, phylogenetically conserved sequence with coll
                                                                                                                                                                                                                                                                                                            Synapsin I (Brain protein 4.1).
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Isogai T., Sugano S.;
CAAT-less, phylogenetically conserved sequence with cell type-specific promoter function.";
                                                             SEQUENCE OF 1-125 FROM N.A. MEDLINE=90368667; PubMed=2118519;
                                                                                                                                                MEDLINE=90243651; PubMed=2110562;
Suedhof T.C.;
                                                                                                                                                                               IISSUE=Brain;
                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata, Euteleostomi;
Mammalia, Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                               Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transport; Protein transport
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EMBL; AK026698; BAB15530.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           106 PRYSREPEMHKT-IKLKYAELAALEEPPKKLEGNKDEPVIAEPPSHLEKYLPDFFSV 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115 RRYSDFAKLQKALLKTFREEIEDVEFPRKHLTGNFAEEMICERRRALQEYLGLLYAI 171
                                                                                                                                                                                              EQUENCE FROM N.A.
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SIMILARITY
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                                                                                                               structure of the human synapsin iol Chem. 265.7849-7852(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AK026698; BAB15530.1; -.
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24; Conservative
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BELONGS TO THE
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A., Fujiwara T., Ono T.,
ri Y., Ota T., Suzuki Y.,
                                                                                                                             protein.";
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EMBL; M58374; AAC41931
EMBL; M58375; AAC41931
EMBL; M58376; AAC41931
EMBL; M58377; AAC41931
EMBL; M58371; AAC40931
EMBL; M55301; AAA60608
EMBL; AM009172; CAA156
PIR; A35363; A35363.
DOMAIN
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                                                                                                      DOMAIN
                                                                                                                                                                           Pfam; PF02078; Synapsin; 1.
Pfam; PF02750; Synapsin_C; 1.
PRINTS; PR01368, SYNAPSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement
                                                                          DOMAIN
                                                                                         DOMAIN
                                                                                                                                   Synapse;
                                                                                                                                                                                                                                                    Genew; HGNC:11494; SYN1.
                                                                                                                                                                                                                                                                    HSSP; P17599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                 PROSITE;
                                                                                                                                                                PROSITE;
                                                                                                                                                                                                                        nterPro;
                                                                                                                       lternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biol. Chem. 265:14932-14937(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: SYNAPSE.
ALTERNATIVE PRODUCTS: 2 ISOFGNES, SYNAPSIN IA (SHOWN HERE) AND SYNAPSIN IB, ARE PRODUCTS: 2 ISOFGNES, SYNAPSIN IB, ARE PRODUCTS: 1T IS SYNAPSIN IB, ARE PRODUCTS BY ALTERNATIVE SPLICING.
PTM: SUBSTRATE OF AT LEAST FOUR DIFFERENT PROTEIN KINASES. IT IS PROBABLE THAT PROSPOPYLATION PLAYS A POLE IN THE REGULATION OF SYNAPSIN IN THE NERVE TERMINAL.
SYNAPSIN IN THE NERVE TERMINAL.
SYNAPSIN IN THE SYNAPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: NEURONAL PHOSPHOPROTEIN THAT COATS SYNAPTIC VESICLE BINDS TO THE CYTOSKELETON, AND IS BELIEVED TO FUNCTION IN THE REGULATION OF NEUROTRANSMITTER RELEASE.
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                                                                                                                                Phosphorylation;
                                                                                                                                                 PS00415; SYNAPSIN_1; 1. PS00416; SYNAPSIN_2; 1.
                                                                                                                                                                                                                       IPR001359; Synapsin.
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Jephory.
Splicing.
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AAC41931.1 JOINED
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705
                                                                                                                                   Neurone;
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B (LINKER
C (ACTIN-
BINDING).
D (FRO-RI
E.
 PHOSPHORYLATION (BY PKA AND CAMKI) PHOSPHORYLATION (BY CAMK2).
                 PHOSPHORYLATION
                                            (PRO-RICH LINKER)
                                                                       (ACTIN-BINDING
                                                                                                                                Repeat; Actin-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         moved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                          AND SYNAPTIC-VESICLE
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16-00T-2001 (Pel 4
16-00T-2001 (Pel 4
15-JUN-2002 (Pel 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HUMAN
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VARSPLIC
CONFLICT
                                                                                                                                                                                              Isogai T, Ora T, Hayashi K, Sugiyama T, Otsuki T, Suzuki Y, Mishikawa T, Nagai K, Sugano S, Takahashi-Fujii A, Hara H., Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Magahari K., Masuho Y., Oshima A.; "NEDO human cDNA sequencing project."; Submitted (AUG-2000) to the EMRL/GenRank/DDBJ databases.
                                               trafficking (By similarity).
-!- SIMILARITY: BELONGS TO THE SORTING NEXIN FAMILY
-!- SIMILARITY: CONTAINS 1 PX DOMAIN.
                                                                                                 Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases. -!- FUNCTION: May be involved in several stages of intracellular
                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21378165; PubMed=11485546;
Teasdale R.D., Loci D., Houghton F., Farlsson L., Glooson F.A.
"A large family of endosome-localized proteins related to sort
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                  Strausberg R
                                                                                                                                                    TISSUE=Kidney;
                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                 TISSUE=Thyroid;
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                                 -!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-7 IS THE INITIATOR.
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24.0%; Pred. No. 1.
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                                                         McLean W H I , Pulkkinen L., Smith F J.D , Pugg E L , Lane E B ,
Bullrich F., Burgeson R.E., Amano S., Hudson D.L., Owaribe K.,
McGrath J.A , McMillan J R , Eady F.A J, Leigh I M , Christiano A M.,
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                                     Uitto J.;
                                                                                                                                                              MEDLINE=96312447; PubMed=8698233;
                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORMS 2 AND 3), AND DISEASE
                                                                                                                                                                                                                                                                                               chromosome localization
                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-96210632; PubMed=8633055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM 1).
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Mammalia, Eutheria; Primates,
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                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 93:4278-4283(1996).
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of plectin causes epidermolysis bullosa with muscular dystrophy.
                                                                                                                                                                                                                                                                                                                                                        .-G., Maercker C., Castanon M J , Hauptmann P , Wiche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AK023332; BAB14/32.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VLPLCEY- LTAHCE - - - - - AAAVEALCAVLLCHECLE 241
                                                                                                                                                                                                                                                                                        (8q24)
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Fied. No. 0.58,
**Ches 96; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    update)
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EMBL; Z54367; CAA01196.1; -.
EMBL; U53204; AAB05427.1; -.
EMBL; U63610; AAB05428.1; -.
EMBL; U63609; AAB05428.1; JOINED.
EMBL; U63609; GAA65765.1; -.
EMBL; X97063; CAA66765.1; -.
HSSP; Q01082; HSKR.
Genew; HGNC: 9069; PLEC1.
                                                                                                                                                                                                                                                                                                                                                                                              MUSCLE, HEART, PLACENTA AND SPINAL CORD.

OPMAIN: THE W-TERMINUS INTERACTS WITH ACTIN, HE C-TERMINUS WITH VIMENTIN, DESMIN, GFAP, CYTOKERATINS, LAMIN B; THE C-TERMINUS WITH AND THE C-TERMINUS CAN BIND INTEGRIN BETA-4.

PTM: PHOSPHOPVLATED BY CDC2; REGULATES DISSOCIATION FROM INTERMEDIATE FILAMENTS DURING MITOSIS (BY SIMILARITY).

INTERMEDIATE FILAMENTS OF THE CAUSE OF EDIDERMOLYSIS BULLOSA WITH MUSCULAR DYSTROPHY (MD. EBS OR EB-MD). AN AUTOSOMAL RECESSIVE DISORDER CHARACTERIZED RY EPIDEPMAL BLISTEP FORMATION AT THE LEVEL. OF THE HEMIDESMOSOME AND ASSOCIATED LATE-ONSET MUSCULAR DYSTROPHY.

ISTMILARITY: CONTAINS 1 ACTIN BINDING DOMAINS.

ISTMILARITY: CONTAINS 1 PLECTIN PEPEATS

ISTMILARITY: CONTAINS 1 PLECTIN PEPEATS

ISTMILARITY: CONTAINS 4 SPECTPIN PEPEATS

ISTMILARITY: BELONGS TO THE PLAKIN OR CYTOLINKER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              deficiency.
Am. J. Path
                                                                                                                                                                                                                                                                                                  use by non-profit modified and this st entities requires a
                                                                                                                                                                                                                                                                                                                                                  the
                                                                                                                                                                                                                                                                                                                                                                             This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MNEDLINE=97049959; PubMed=8894687; Pulkkinen L. Smith F.J.D., Shimizu H., Murata S., Yaoita H., Hachisuka H., Nishikawa T., McLean W.H.I., Uitto J.; "Homozygous deletion mutations in the plectin gene (PLEC1) in patients with epidermolysis bullosa simplex associated with late-onset
         Pfam; PF00307; CH; 2.
Pfam; PF00681; Plectin; 19.
Pfam; PF03501; S10 plectin; 1.
SMART; SM00033; CH; 2.
                                                           InterPro; IPR001589; Actbind_actnin.
InterPro; IPR001715; Calponin-like.
InterPro; IPR001101; Plectin_repeat.
InterPro; IPR005326; S10_plectin.
InterPro; IPR002017; Spectrin.
                                                                                                                                                                                                                                                                                         or send an
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Bauer J.W., Pouan F. Kofler B., Pezniczek G.A., Kornacker I.,
Muss W., Hametner R., Klausegger A., Huber A., Pohla-Gubo G.,
Wiche G., Uitto J., Hintner H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21090821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        muscular dystrophy."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA cloning and genomic organization Genes Dev. 10:1724-1735(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANT MD-EBS 1003-GLN--ALA-1005 DEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  compound heterozygous one amino-acid insertion/nonsense mutation in e plectin gene causes epidermolysis bullosa simplex with plectin
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MICROFILAMENTS AND ANCHOPS INTERMEDIATE FILAMENTS TO DESMOSOMES OF MICROFILM TO DESMOSOMES OF HEMIDESMOSOMES. COULD ALSO BIND MUSCLE PROTEINS SUCH AS ACTIN TO MEMBRANE COMPLEXES IN MISCLE, MAY BE INVOLVED NOT ONLY IN THE CROSSLINKING AND STABILIZATION OF CYTOSKELETAL INTERMEDIATE FILAMENTS NETWORK, BUT ALSO IN THE PROJUCTION OF THEIP DYNAMICS. SUBUNIT: HOMODIMER OF HOMOTETRAMER, ALTERNATIVE POPOLYTIS: 3 ISOPOMES; 1 (SHOWN HERE), 2 AND 3; APE PRODUCED BY ALTERNATIVE SPLICING.

PRODUCED BY ALTERNATIVE SPLICING.

TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGHEST LEVELS IN MICROFILM AND CONTACT.
                                                                                                                                                                                                                                                                                                                           s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                 and this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.ish-sib.ch/announce/
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                                                                                                                                                                                                                                                                                         email to license@isb-sib.ch).
       CONFLICT
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SMART; SM00150; SPEC; 5.
SMOSITE; PS00010; ACTININ 1;
PROSITE; PS00020; ACTININ 2;
PROSITE; PS00021; CH; 2.
PROSITE; PS00021; CH; 2.
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4539
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      185
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L -> LL (IN MD-EBS).
/FTId=VAR 011336.
MISSING (IN MD-EBS).
/FTId=VAR 011337.
/FTId=VAR 011337.
S -> F (IN REF. 2).
H -> N (IN REF. 2).
H -> V (IN REF. 2).
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RPGPEPAAT -> MSGEDAEVBAVSEUVSNGSGGSSSSPSDG
TLPWNLGKTQRSRRSGGGAGSNGSVLDPAERAVIRIA (IN
ISOFORM 2 AND ISOFORM 3).
MISSING (IN ISOFORM 3).
                                                                                                                                                                                                                                                                   SIMILARITY)
4 X 4 AA TA
                                                                                                                                                                                           GVTNLQVMRAMASLRARGLVRETFAWCHFFWYLTNEGIAHL
RQYLHLPPEIVAASL@EVERPVAMVMPARRTPHV@AV@GPL
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BINDING TO INTERMEDIATE FILAMENTS
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Euvaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                      OSUNNIE; UMYSZ7; UMSEWM9; OSUNNIE; UMYSZ7; UMSEWM9; OSUTT-2001 (Rel. 40, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                 NVWITH
        Euwaryota; Metazoa;
                                Sorting nexin 7.
                                                                          NAMUH LXNS
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                Homo sapiens (Human)
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                                                                                                                   752 LESIHSFVAAATKELMWLNEKEEE 775
                                                                                                                                  270 LDAMVRLAYALGKDFVTLQERLEE 293
                                                                                                                                                  695 HRGLHQSIEEFQA---KIEPARSDEGQLSPATRGAYPDCLGPLDLQYAKLLNSSKAPLRS 75:
                                                                                                                                                                  237 HRDLDRFAEAFAAGERALQFLQAREGH---
                                                                                                                                                                                  635 APATQVAQVTLQSVQRRPELEDSTLPYLQDLLAWVEENQHEVDGAEWGVDLPSVEAQLGS 694
                                                                                                                                                                                                    222 CPAAAV------
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                                                                                                                                                                                                                                                                      128
                                                                                                                                                                                                                                                                                                                    404 DVQDGVRAN-----ELQLRWQEYR---ELVLLLLQWMRHHTAAFEERRFPSSFEEIEIL 454
                                                                                                                                                                                                                                                                                                                                      44 DTHSGLSSNSSMTTRELQQYWQNQKCPWKHVKLLFEIA---SARIEERKV------ 90
                                                                                                                                                                                                                                   FLDFLTRPE--LREAFG---CLPAGQYPRALELLLPVLPLQEKLTA----
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                                                                                                                                                                                                                                                   LEREKOLRSEFERLECLORIVTKLOMEAGLCEEOLHOADALLOSDIRLLAAGKVPORAGE 574
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                                                                                                                                                                                                                                                                                                                                                               Similarity
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20 3%;
       Chordata;
                                                                                                                                                                                                                                                                                                                                                     51; Mismatches 109; Indels 146; Gaps
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PROSITE, PS50195; PX; 1.
Transport; Protein transport
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SUMMARI

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Drosophila melanogaster (Fruit fly)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---HVKLLFEIASAPI-----EEPKVSKFVVYQIIVIQTGSF-SNNKAVLEPPY 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            326 VV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37252 MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.7%; Score 210; 27.6%; Pred. No. 9
                                                    Last annotation update)
                                                                                       Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 5.6e-
8; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6BA23C09D7F1:A62 CFC64;
                                                                                                                                                                                      295 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ŗ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----LPLYIPLLH 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68;
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RX MEDLINESCOPPEDS, Chimmer M., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt P. M., Hoskins R.A., Galle R.F.,
RA Gaorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Gaorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Handon R.C., Pogers Y.-H.C., Blazej P.G., Champe M., Pfeiffer B.D.,
RA Handon R.C., Pogers Y.-H.C., Blazej P.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Boyle C., Baxter E.G., Helt G., Neison C.P., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K Y., Benos P.V., Berman B.P., Bhandari D., Botchter P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Bothkov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Bothkov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Bothkov B.C., Dunn P.
RA Charry J.M., Cawley S., Dahike C., Davenport L.B., Davise P.,
RA Charry J.M., Cawley S., Dahike C., Davenport L.B., Davise P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., House C.,
RA Hostin D., Houston K.A., Howland T.J., Harris M., Melsen D., Lai Z.,
Laing Y., Lin X.,
RA Hostin D., Houston K.A., Howland T.J., Mariy P. M., Phelefi A.,
RA Merkulvo G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulvo G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue R.C., Siden-Kiamos I., Sirpson M., Skugski M.P., Smith T.,
RA Mander E., Strading A.C., Stapleton M., Stugski M.P., Smith T.,
RA Mander E., Strading A.C., Stapleton M., Stugski M.P., Smith T.,
RA Mander E., Stapleton M., Meissenbach J.,
RA Mander E., Stapleton M., Meissenbach J.,
RA Mander E., Stapleton M., Meissenbach J.,
RA Mander E., Stapleton M., Ston
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Best Local :
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SMART, SM00312; PX;
SEQUENCE 295 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE003582; AAF51213.1; -
FlyBase; FBgn0031457; CG3077.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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    185
                                             195
                                                                                        135
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                                                                                                                                                                                                                                                                                                     37
                                                                                                                                                                         75
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                                                                                                                                                                                                                                                             16
LIKIYMNPSPPVILITIC----PI-VAACTSSPVPHHAAERWALLALSRFETLCDIDL----
                                                                                                                                                                                                                                                                                                     PGPDGHLDT----HSGLSSNSSMTTFELQQ-YWQN-QKCPWK-----HVKLLFEIASARI
                                                                                                                                                                       MPPDGEDVKIKFFVVYELTVKQDGATEDTQPAKIEFRYTDFRELYLGLKRQHPAEMANKY 134
                                                                                                                                                                                                                ----EERKVSKFVVYQIIVIQTGSF-DNNKAVLERRYSDFAKLQKALLKTFREEIEDVE
                                                                                                                                                                                                                                                          PGPD-ELDSPAIEAAALDIPPPESDKALQKGVWERATSAEYKPTTDGSTVLRFDILLAHI 74
                                        LPAGQYPFALELLLRVLPLQEKLTAHCPAAAVP-----ALCAV----LLCHRDLDRPA 244
                                                                                 FPAKVIMGNEKSELIGERSAAFRASI.-----TACQELDERRNEMAIPILENCERL 184
                                                                                                                            FPRKHLTGNFAEEMICERRRALQEYIGILYAIPCVRPSPEFLD----FLTPPELPEAFGC
                                                                                                                                                                                                                                                                                                                                                ; 08
                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PX;
                                                                                                                                                                                                                                                                                                                                                                                                                                33532 MW; 7D7805C001B0F31D CRC64;
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27 7%,
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                                                                                                                                                                                                                                                                                                                                                                  Score 185.5; I
                                                                                                                                                                                                                                                                                                                                              Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                       DB 5;
                                                                                                                                                                                                                                                                                                                                                                                       Length 295;
                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                              69;
                                                                                                                                                                                                                                                                                                                                          Gaps
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, BC019823; AAH19823.1; -.
InterPro; IPR001683; PX.
Pfam; PF00787; PX; 1
SECUENCE 199 AA; 21872 MW; D46D7CD4E0D671CC CRC64,
                                                                                                                                                                      MEDLINE=97397562; PubMed=9253601;
Gurus C , Agarwal S K , Manickam P , Olufemi S.-E., Crabtree J.S.,
Weissemann J.M., Kester M., Kim Y.S., Emmert-Buck M.R., Liotta L.A.,
Spiegel A.M., Boquski M., Roe R A., Collins F S., Burns A L.,
Marx S.J., Chandrasekharappa S.C.,
"A transcript map for the 2.8-Mb region containing the multiple
endocrine neoplasia type 1 locus.";
Genome Pes 7.725.735(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    014612;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Hypothetical 17.8 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae,
EMBL; AF001435; AAB81205.1; -.
InterPro; IPR001683; PX.
Pfam; PF00787; PX; 1.
SMART; SM00312; PX; 1.
Hypothetical protein.
SEQUENCE 152 AA; 17784 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAP-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to chromosome 20 open reading frame 161.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31 GPD-LP------HPGPDGHLDTHSGLSSNSSMTTRELQQYWQNQKCRWKHVKLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       _TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEVTSANVVKDPPSKYVLYTLTVIGPGPGPCQPAQISPPYSDFEPLHPNIQPQFEGFMAA 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISFPQSH 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VEFPRKH 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEIASARIEERKVSKFVVYQTIVIQTGSFDNNKAVLEPRYSDFAKLQKALLKTFREEIED 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GPDQLPLGDGTSGEDAERSPPPDGQW------GSQLLARQLQDFWKKSRNTLAPQRLL 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINAPY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.6%; Score 174.5; DB 4; Length 199; 33.1%; Pred No. 3 3e-07;
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2B3AF6C5A77CBREF CFCK4;
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RESULT 7
Q9XIM1
ID C9XI
AC Q9XI
DT 01-N
DT 01-D
DE AL2g
GN AT2G
OS AFAA
OC Sper
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Q91WE1
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Q9
DT
Q9
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Q1
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Best Local S
Matches 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local
                                                                                                                                                                             01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 13, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q91WE1;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
Hypothetical 37.7 kDa protein.
                          Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
                                                                                                                               AT2G15900
                                                                                                                                                      At2g15900 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00787; PX; 1.
Hypothetical protein.
SEQUENCE 337 AA; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_
                                                                                                                                                                                                                                                                                   Q9XIM1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; BC016091; AAH16091.1; -. MGD; MGI:1916274; 1500032B08Rik. InterPro; IR001683; FX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.; Strausberg (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q91WE1
                                                                                                                                                                                                                                                                                                                   DOXIM1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=EYE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1500032B08RIK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              194 GCLRAGQYPRALELL--LRVLP 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 -- RGGEVTRPLEVSRDLHILP 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 --- RGGEVTRPSEVSRDLRILP 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         σ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEIASARIEERKVSKFVVYQIIVIQTGSFDNNKAVLERRYSDFAKLQKALLKTFREEIED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YTVSDERTHEKGYTEYKVTAQFISKKPEDVKEVVVWKEYSGERKLHGDLAYTHENLFER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LEEFPAFPRAQVFGRFEASVIEEPPKGAEDLLRFTVPIPALNNS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VE----FPRKHLTGNFAEEMICERPRALQEYLGLLYAIRCVPRSPEFLDFLTPPELREAF 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YTVSDPRTHPKGYTEYKVTAQFISKKDPEDIKEVVVWKRYSDFRKLHGDLAYTHRNLFRR 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TaxID=10090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCLRAGOYPRALELL -- LRVLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LEEFPAFPRAQVFGRFEASVIEERRKGAEDLLRFTVHIPALNNS------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEIASARIEEPKVSKFVVYQIIVIQTGSFDNNKAVLERRYSDFAKLQKALLKTFREEIED 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 27.5%; Fred. No. 0.00
39; Conservative 24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AND RETINA;
                                                                                                                                                                                                                                                                                                                PRELIMINARY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
Brassicales, Brassicaceae, Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37742 MW; 743923E18ED9EF4B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.4%; Score 122, DB 11;
27.5%; Pred. No. 0.021;
ive 24; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.4%, Score 122, DB 4, Length 152; 27.5%; Fred. No. 0.0075;
                                                                                                                                                                                                                                                                                                                FET,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 337,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18;
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                                    Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local (
                                                                                                                           STRAIN=972;
McDougall R.C., Rajandream M.A.,
                                                                                                                                                                                                                                                                                    01 MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN 2002 (TrEMBLrel. 21, Last annotation update)
Hyporhetical 117.0 kDa protein C16All 04 in chromosome
SPCC16All.04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDITINE-20083487; PubMed-10617197;
Lin X., Faul S., Pounsley S. D., Shea T. P., Benito M.-T., Town C. D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchim K.A., Lee J. J., Ponning C. M., Foo H., Moffat K.S.,
Cronin L.A., Shen M., VanAken S.E., Imayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T. H., Goodman H.M., Somerville C.P.,
Adams M.D., Freits D., Nierman W.C., White O., Eisen J.A.,
Copenhaver G.P., Preits D., Nierman W.C.,
Salzberg S.L., Fraser C.M., Venter J.C.;
"Sequence and analysis of chromosome 2 of the plant Arabidopsis
Pfam; PF00787;
Pfam; PF02194;
                                                                           EMBL; ALIO9957; CARS3076 1; -
                                                                                                                                                                                                                                   Eukaryota; Fungi; Ascomycota; Schizosaccharomycete Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                   Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; [PR001114; PX_assoc
Ptam; pep00787; PX; 1
Ptam; pep00787; PX; 1
Ptam; pep02194; PXA; 1
SMART; SM00312; PX; 1
SMART; SM00313; PXA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AC006438; AAD41976.1; -. InterPro; IPF001683, FX.
                                                                                                            Submitted (AUG-1999) to the EMBL/GenBank/DDBJ
                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                         Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                               01 MAY-2000
                                                                                                                                                                                                                                                                                                                                                                   COUSNI;
                                                                                                                                                                                                                                                                                                                                                                                  Q9USN1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-CV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 402:761-768(1999).
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                                  InterPro;
                                               InterPro;
                                                              InterPro; [PROO1683; PX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lin X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     554 DV---ENKTWEVKRRYSNEERLHROL-----KEIPNYNLOLPPKRIESSSTEDAFVHROC 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  503 HNDNYICDNKSOSIVIHKEGOHCLKLKCE-----VLGAYFEKOGSKSFAVYSIAVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                            606 IQLDKYLQDLLCIANVAEQHEVWDFLSAASKNYSFG 641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         159 RALQEYLGLLYAIRCVRRSREFLDFLTPPELPEAFG 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HIDTHEGLSSNSSMTTRELQQYWQNQKCRWKHVKLLFEIASARIEERKVSKFVVYQIIVI 101
                                                                                                                                                                                                          TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QTGGPDWWKAVLERFYSDFAKLQKALLKTFPEETE--DVEFPRKHLTGNFAEEMIGERR- 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FROM N.A.
 IPR003114; PX_assoc.
IPR000342; Pegl Gprotein.
0787; PX; 1.
2194; PXA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COLUMBIA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            952 AA,
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                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          108995 MW, 1F42F8ED1848R098 CPC64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.1%; Score 117; DR 26.3%; Pred. No. 0.2;
                                                                                            MDM1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25;
                                                                                                                                                                                                                                                     Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                          Barrell B.G.,
                                                                                                                                                                                                                                                                                                                                                                                  1010 AA
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                                                                                                              databases
                                                                                                                                           Zimmermann
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RESULT 9
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Best Local
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01-DEC-2001 (
01-DEC-2001 (
01-JUN-2002 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
CARBOHYD
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CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                    Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsert V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K. Yu C., Lewis S. E., Rubin G.M., Celniker S.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00615; RGS; 1.
SMART; SM00312; PX; 1.
SMART; SM00313; PXA; 1.
SMART; SM00313; PGS; 1
  ATP-binding; 11
                    ProDom; PD000001; Euk_pkinase; 1.
PROSITE, PS50C11, PROTEIN_KINASE_DOM; 1.
                                               Ffam, FF0C069, pkinase; 1. Ffam, PF00787; PX; 1.
                                                                             FlyBase; FBgnC033244, CG8726.
InterPro; IPR000719; Euk_pkinase
                                                                                                                                                                                     STRAIN=BERKELEY;
                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                    NCBI_TaxID=7227;
                                                                                                                                                                                                                                Pterygota; Neoptera, Endopterygota, Dir
Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                          Bukaryota; Metazoa, Arthropoda, Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera, Endopterygota, Diptera, Brachycera, Musc
                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                              CG8726
                                                                                                                                                                                                                                                                                                                                                 Q95RK3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAPBOHYD
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                                                                                                                                                                                                                                                                                      LD23236p.
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                                                                     InterPro; IPR000719; Euk
InterPro; IPR001683; PX.
                                                                                                                                                                                                                                                                                                                                                                                                                          170 AIRCVKRSREFLDFLTRFELR
                                                                                                                                                                                                                                                                                                                                                                                                                                                736 WMV-ARRYREFAELHKQIKQTY-PGVPSIKFFQKSIITSLNKNVLEYPRGALEEYLQSIF 793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    110 KAVLEFRYSDFAKLOKALLKTFREETEDVEFPRKHLTGNFAEEMICERPPRALGEYLGLLY 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              681
                                                                                                                                                                                                                                                                                                                                                                                                     794 RMPEVODSEMLEMELSOCHTTAROMEREPOREWOLLEVI 835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SH PELZOYMONOKOPMKHYKLLFEIASARIEEPKVSK-----PVVYOIIV ILTOSEDNN 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POPDOYMSOEE - -
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                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 19, (TrEMBLrel. 19, (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
Transferase.
50 AA; 50748 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116992 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 116; DB 3; Pred. No. 0.27;
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    D1BABF8CEFE27E15 CRC64;
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                                                                                                                                      Phouanenavong S., Wan K.,
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                                                                                                                                                                                                                                            Brachycera, Muscomorpha;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Probable flagellar assembly protein FLIH.
FLIH OR RSP0392 OR RS00820.
Palstonia solanocommunications
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Bilault A., Brottier P., Camus J.C., Cattolico L., Arlat M., Choisne N., Claudel-Renard C., Cunnac S., Demange N. Gaspin C., Lavie M., Moisan A., Robert C., Saurin M., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A.; Weissenbach J., Boucher C.A.; "Genome sequence of the plant pathogen Ralstonia solanacearum."; Nature 415:497-502(2002).; "Levis M., A.646078; C.AD17543.1; "...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Palstonia solanacearum (Pseudomonas solanacearum)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8XSS5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmid megaplasmid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21681879; PubMed=11823852;
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SEQUENCE 248 AA; 26993 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000563; Flag_FliH.
Pfam; PF02108; FliH; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37 LLRVWRGASNKNYWTVLRRYNDFDRLDKSL----RVSGIELPLPRKRIFGNMRPEFIAER 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98 IIVIQTGSFDNNKAVLERRYSDFAKLQKALLKTFREEIEDVEFPRKHLTGNFAEEMICER 157
                                                                                                                                                                                                                                                                                                                                                                                                                                           126 ALLKTFREETEDVEFPRKHLTGNFAEEMICERRRALQEYLGLLYAIRCVRRSREFLDFLT 185
                                                                                                                                                                                                                                                 134 -----GALRA--QPE-----RILPLVREVLGDAPTAPAPAMLRVHADDAELIRQAL 177
                                                                                                                                                                                                                                                                                                                186 RPELREAFGCLRAGQYPRALELLLRVLPLQEKLTAHCPAAAVPALCAVLLCHRDLDRPA- 244
                                                                                                                                                                                                                                                                                                                                                                                      100 ALMOSVREAID----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16 HEWEE ----TDFVPCAELAAAAAAP--PPPPPEPEPEPEIS-----EEEWO 57
                                                           293 ESQL 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66 NQKCRWKHVKLLFEIASARIEERKVSKFVVYQIIVIQTGSFDNNKAVLERRYSDFAKLQK 125
237 AERV 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 -----AMLEAELANARDEGRRDGFAQGFQ-----DGFEQGR----FQGEEDSRQIA 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 HPGSPGCMGPITQCTARTQQEAPATGPDLPHPGPDGHLDTHSGLSSNSSMTTRELQQYWQ 65
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                                                                                                                       GTELAÄÄGWTLVVDAAIERGGCRVQTREGET-DATLQTRWAELTRÄLGRDTAWIASERVE 236
                                                                                                                                                                                      --EAFAAG-----ERALORLOAREGHRYYAPLLDAMVRLAYALGKDFVTL-QERLE 292
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30.1%; Pred. No. 0.11;
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                                                                                                                                                                                                                                                                                                                                                                                          ---QMNGSVAEELV------GL----ALQLAQQFLR--- 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.0%; Score 115; DB 1
24.0%; Pred. No. 0.056;
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RESULT 11
Q9W488
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01-MAY-2000
01-JUN-2002
                                                                         Matches
                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20196006; PubMed=10731132;
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                                                                                                                                                                                                                               InterPro; IPR001683; PX.
InterPro; IPR000189; RA_domain.
pfam; PF00787; PX; 1.
smART; SM00312; PX; 1.
                                                                                                                                                                                                                                                                                                                                                                          FlyBase; FBgn0029794; CG3138.
                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; Q12923;
                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE003435; AAF46070.1; -.
23 TOOFAFATGFDLFHFGFDGHLDTHSGLSSNSSMTTRELQQYWQNQXCFWKHVKLLFEIAS 82
                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TaxID=7227;
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                                                                         44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                         431 AA; 49535 MW; 9E5F03709DA2F697 CRC64;
                                                                            Conservative
                                                                                                          6.9%; Score 114.5;
25.9%; Pred No. 0.1
                                                                                    20;
                                                                                    Mismatches
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                                                                                                                        0.12;
                                                                                       63; Indels
                                                                                                                                                             Length 431;
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RESULT 12
Q9CRB0
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RA MEDLINE-21085660; PubMed=11217851;
RA Kawai J. Shinagawa A. Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Kawai J. Shinagawa A., Shibata K., Yoshino M., Wananaka I.,
RA Arabawa T., Hara A., Fubunishi Y., Konno H., Adachi J., Pukuda S.,
RA Arabawa T., Hara A., Fubunishi Y., Konno H., Kondo S., Yamanaka I.,
RA Arabawa T., Hara A., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Kaito T., Okazaki Y., Gojobori T., Bono H.,
RA Kadota K., Marsuda H. A., Ashburner M., Batala V., King B., Kochiwa H.,
RA Kudhi D., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kudhi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kudhi R., Staubi F., Sruzuki F., Tomita M., Wagner I., Washio T.,
RA Schriml I.M., Staubi F., Sruzuki F., Tomita M., Wagner I., Washio T.,
RA Sakai K., Okido T., Puruno M., Aono H., Baldarelli B., Barsh G.,
RA Hlake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Sakai K., Okido T., Puruno M., Hono D. A., Kamiya M., Lee N. H.
RA Hlake J., Boffelli D., Hofmann M., Hume D. A., Kamiya M., Lee N. H.
RA Gustincich S., Hill D., Hofmann M., Hume D. A., Kamiya M., Lee N. H.
RA Nordone F., Ring B., Ringwald M., Rohitaye T., Sakamato N.,
RA Sasaki H., Saro K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Wynslaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Mynslaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RT Hayashizaki Y.,
RT H. Hayashizaki Y., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RT Hayashizaki Y., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN 2002 (TrEMBLrel. 21, Last sequence update)
5730433116Rik protein (2810011K15Rik protein).
5730433116RIK OR 2810011K15RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AK012711, BAB28427.1, ...
MGD; MGI:1916476; 2810011K15Pik
MGD; MGI:1922957, 9730433116Fik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
Eukaryota; Metazoa; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9CRB0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AK017610; BAB30838.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Functional annotation of a full-length mouse cDNA collection."; Mature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria; Podentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9CRB0;
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPPOOL683; PX.
Pfam; PF00787; PX; 1
111 AESC 114
                                            192 AFGC 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124
                                                                                                                                  139 EFPRKHLTGNFAEEMICERPRALGEYLGLLYAIPCVPPSPE----FLDFLT----RPELRE 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14) KHLTGNF----AEEMICERPRALQEYLGLLYAIRCVRRSREFLDFLTRPE 188
                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                      57 EIPSKHVR-NWVPKVLEQRRQGLETYLQAV----ILENEELPKLFLDFLNVRHLPSLPK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 TOQEADRLEPQ------EDQSGYSYIDYSDKRSLP-----ISIPD 74
                                                                                                                                                                                                                                  80 IASARIEERKVSK-FVVYQIIVIQTGSFDNNKAVLERRYSDFAKLQKALLKTEREEIEDV 138
                                                                                                                                                                                        ŗ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YGIVNRNGERYIVFNIHMA-----GPQLCSPRYREFANLHSLL----PKEFSGFNFPK 123
                                                                                                                                                                                   IPSFRHEDSDIEPGYTVFKIEVIMNG----RKHFVEKRYSEFHALHKKLKKC----IKTP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - LPGKWPFQLSEQQLDTPPPGLEQYLEKVCAVRVIAESDAVQDFLTDTE 171
                                                                                                                                                                                                                                                                                 39;
                                                                                                                                                                                                                                                                                                                                                                                                   SM00312; PX;
                                                                                                                                                                                                                                                                                                                                                                            169 AA,
                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                     6.8%; Score 113;
31 5%; Pred No (
                                                                                                                                                                                                                                                                                                                                                                       19652 MW; 076416D452392D69 CRC64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                               23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                  0 051;
                                                                                                                                                                                                                                                                                                                         DB 11;
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                                                                                                                                                                                                                                                                               40,
                                                                                                                                                                                                                                                                                                                           Length 169;
                                                                                                                                                                                                                                                                               Indels
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(1
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RESULT 13
Q90990
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Q941X3
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Best Local S
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                                                                                                                                                                                         Q941X3, PRELIMINARY;
Q941X3,
01-DEC-2001 (TYEMBLYEL 19,
01-DEC-2001 (TYEMBLYEL 19,
01 MAR-2002 (TYEMBLYEL 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON_TER
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Nonerythroid alpha-spectrin mRNA (Fragment).
Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPP002017; Spectrin
Pfam; PF00435; spectrin; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, M11053; AAA49074.1,
HSSF; P07751; 1AJ3.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryzea.
                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                            Oryza sativa (Rice)
                                                                                                                                    B1088C09
                                                                                                                                                     B1088C09.3 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00150; SPEC; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nonerythroid spectrin.";
Proc Natl Acad. Sci U S.A 82.5671-5675(1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hughes S.H., Barker J.E.; "Remarkable homology among the internal repeats of erythroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=85298223; PubMed 3862089;
Birkenmeier C_S., Rodine D M., Repasky E.A., Helfman D M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       090990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              370 AAKHIQSKAIEVRHASLMKRWHQIILAHSAARKKILLEAQEHFRKVEDLFLTFAKKASAFN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      143 PAIQGVLDTGKKLSDDNTIGKEEI@@RLARFVDHWKELKQLAAARGQRLEESLEY@FVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  282 KDEVTLOERLEE 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      310 ADVVESWIGEKENSEKTEDYGFFESSVØTELTFØRTFFAGEØAFVÆRGIANITALKFQLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37 PGPPGHLPTHSGLSSNSSMTTFFELQQYWQNQKCPWKHVKLLFEIASARIEER KVSKFV 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KKNNHHVENITAKMKGLKGKVSDLEKAAAQPFAKI.DE------NSAFI QFNWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PELREAF-----GCLRAGQYPRALELLLRVLPLQEKLTAHCPA-----AAVPALCAVLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KTFPEEI EDVEFPPKHLTGNFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     473
473 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative 44; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - HRDIDSFASAFAAGEFALGE LOAFEGHEYYATILIDAMVKLAYALG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             473
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21.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .....VYQIIVIQTGSFDNNKAVLERRYSDFAKLQKALL 128
                                                                                                                                                                                             Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 111;
Pred. Nc. 1.
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                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                           577 AA
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es 134; Indels
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Q91WB6
ID Q91WB
AC Q91WB
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AC Q91WB
DT 01-DE
DT 01-DE
DT 01-DE
DT Sinin
OC Eukar
OC Musm
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Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, BAC
T clone:B1088C09.";

T clone:B1088C09.";

L Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.

R EMBL; AP003734; BAB68097.1;

JR InterPro; IPR001064; Crystallin.

JR InterPro; IPR001064; Crystallin.

JR InterPro; IPR001683; PX.

DR Pfam; PF00787; PX; 1.

DR Pfam; PF00787; PX; 1.

DR PFCSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN 1.

SQ SEQUENCE 577 AA; 62866 MW; A3EF868B68FCB31D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local
                                   Query Match
Best Local S
         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q91WB6;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to hypothetical protein FLJ20335.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata,
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae
                                                                                                                                                                                                                                                                                                                                     EMBL; BC016131; AAH16131.1; -. InterPro; IPR000719; Euk pkinase. InterPro; IPR001683; PX. InterPro; IPR003124; WH2.
                                                                                                                      ProDom; PD000001; Euk_pkinase; 1.

PPOSITE; PS5011; PSOTEIN FINASE DOM; 1.

ATP-binding; Hypothetical protein; Transferase.

SEQUENCE 582 AA; 65201 MW, ED55496B61F2E9AA CRC64;
                                                                                                                                                                                                                                               Pfam; PF00069; pkinase; 1. Pfam; PF00787; PX; 1. Pfam; PF02205; WH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=SALIVARY GLAND;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=CV. NIPPONBARE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -IPGSGSYFSYLITTRAADGGLERVRREEPDVVALADRLAAAYRGLEVPARRDKSIVEGQ 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KVSKFVVYQIIVIQTGSFDNNKAVLERRYSDFAKLQKALLKTFR-----EEIEDVE 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------DGHLDTHSGLSSNSSMTTRELQQYWQNQKCPWKHVKLLFEIASARIEER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ASPEHPGSPGCMGPITQCT-----ARTQQEAPATGPDLPHPGP------
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      32; Conservative
                                      Similarity
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24.5%; Pred. No. 0.39;
6.6%; Score 109.5; Di
36.4%; Pred. No. 0.48;
tive 10; Mismatches
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                                                            DB 11;
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      39; Indels
                                                         Length 582;
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   7;
Gaps
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Search completed: April 20, 2003, 14:07:05
Job time : 89 secs

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Database :
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Maximum DB seq length: 200000000
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Perfect score:
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1. /SIDS2/gogdata/geneseq/geneseqp-emb1/AA1980.DAT:*
2. /SIDS2/gogdata/geneseq/geneseqp-emb1/AA1981.DAT:*
3. /SIDS2/gogdata/geneseq/geneseqp-emb1/AA1982.DAT:*
4. /SIDS2/gogdata/geneseq/geneseqp-emb1/AA1983.DAT:*
5. /SIDS2/gogdata/geneseqf-emb1/AA1983.DAT:*
5. /SIDS2/gogdata/geneseqf-emb1/AA1984.DAT:*
6. /SIDS2/gogdata/geneseqf-emb1/AA1986.DAT:*
7. /SIDS2/gogdata/geneseqf-emb1/AA1987.DAT:*
8. /SIDS2/gogdata/geneseqf-emb1/AA1988.DAT:*
9. /SIDS2/gogdata/geneseqf-geneseqp-emb1/AA1988.DAT:*
                  US-09-816-697A-2
1650
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Listing first 45 summaries
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//SIDS2/gcgdata/geneseq/geneseqp.emb1/AA1990.DAT:
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/SIDS2/gcgdata/geneseq/geneseqp.emb1/AA1990.DAT:
/SIDS2/gcgdata/geneseq/geneseqp.emb1/AA1991.DAT:
/SIDS2/gcgdata/geneseq/geneseqp.emb1/AA1993.DAT:
/SIDS2/gcgdata/geneseq/geneseqp.emb1/AA1993.DAT:
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/SIDS2/gcgdata/geneseq/geneseqp.emb1/AA1994.DAT:
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/SIDS2/gcgdata/geneseq/geneseqp.emb1/AA1999.DAT:
/SIDS2/gcgdata/geneseq/geneseqp.emb1/AA1999.DAT:
/SIDS2/gcgdata/geneseq/geneseqp.emb1/AA2001.DAT:
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1079.672 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Novel signal trans	Novel human diagno	Drosophila melanog	Human immune/haema	Novel human diagno	Human cancer cell	Human immune/haema	Human ORFX ORF2831	Amino acid sequenc	Amino acid sequenc	Description

WPI, 2001-616502/71

Lorenz M,

Kriz R, Weich N,

Shaw GD;

5.5 5.8 2930 22	4 95.5 5.8 2392 22	3 95.5 5.8 2392 22	2 95.5 5.8 1911 22	1 95.5 5.8 813 22	0 95.5 5.8 784 22	9 95.5 5.8 259 22	8 96 5.8 1191 23	7 96 5.8 595 21	6 96.5 5.8 512 22 AAM4052	5 96.5 5.8 455 2	4 96.5 5.8 447 22	3 97 5.9 270 22 NAB9556	2 97 5.9 270 22 AAE0476	1 97.5 5.9 491 22 ABB6069	0 98 5.9 565 22 ABB6266	9 98 5.9 278 22	8 98 5 6.0 165 22 AAU1743	7 98.5 6.0 66 22 AAU1761	6 99 6.0 141 22 AAU1747	5 99.5 €.0 714 22 AAM4111	4 99.5 €.0 705 22 AAM3932	3 99.5 6.0 649 22 AAB6568	2 99.5 6.0 156 22 ABG2289	1 100.5 6.1 578 23 ABB9732	0 100.5 6.1 577 22 AAE0277	9 100.5 6.1 344 23 AAE2338	8 103.5 6.3 320 22 ABG0765	7 103.5 6.3 245 22 ABG2024	6 107 6.5 520 22 ABB6149	5 107.5 6.5 166 22 ABG2289	4 108.5 6.6 141 22 AAU1748	3 112.5 6.8 541 23 ABB0815	12.5 6.8 168 21	1 114.5 6.9 431 22 ABB5966
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AAB81485	AAB84759	AAB84758	AAG67401	AAE00684	AAE00685	AAU68540	ABB97940	AAB43303	AAM40526	ABB11613	AAG74174	MABarras	AAE04763	ABB60691	ABB62665	AAU17486	AAU17438	AAU17617	AAU17470	AAM41114	MAM3 9328	AAB65680	ABG22890	ABB97328	AAE02775	AAE23382	ABG07654	ABG20248	ABB61499	ABG22895	AAU17481	ABB08158	AAB45187	B5966
Atr 2 solve	se defective	ΙP	d sequen	TMF recepto	TNF recepto	novel cy		Human OPFX OPF3067	Human polypeptide	Human sorting nexi	colon ca	protein	vesic	phila me	Drosophila melanog	l signal	lsignal	signal		Human polypeptide	n polyp	l prote	1 human		PPO-C	n intra	1 human	human	ophila	l human dia	signa.	cytoskeleto	creteo	Drosophila melanog

ALIGNMENTS

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RESULT 1
AAG79225
ID PAG7
XX AAG7
XX AAG7
XX AAG7
XX AMIT
XX AMIT
XX Huma
DE Amit
XX PSGII
KW PSGII
KW PSGII
KW Immu
KW Ocall
XX Home
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                                                                                                                                                                                                                                                                                                                     Human; P-selectin glycoprotein ligand binding protein; PSGL-1 binding protein; selectin ligand interactor cytoplasmic-1 protein; SLIC-1 protein; signal transduction; cytoskeletal organization; immune response; inflammatory response; cell adhesion; cell migration; cell activation; cell growth; cell differentiation; cell proliferation; immune system disorder; cardiovascular disorder; haematopoietic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG79225,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAG79225 standard; Protein; 316 AA.
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                                                                                                                                                                                                                             WO200173028-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amino acid sequence of a human PSGL-1 binding protein.
                                                                         (GEMY ) GENETICS INST INC.
                                                                                                             24-MAR-2000; 2000US-192104P
                                                                                                                                                 23 MAR-2001, 2001WO-US09469
                                                                                                                                                                                         04-OCT-2001.
                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                       thrombotic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a human P-selectin glycoprotein ligand (MSGL-1) binding protein. The protein is a member of the selectin liquid interactor cytoplasmic (SLIC-1) family. The SLIC-1 polynucleotides and polypeptides are useful as targets for developing modulating agents to regulate a variety of cellular processes such as signal transduction, cytoskeletal organization, immune and inflammatory responses, inter- and intra-cellular communication, adhesion, migration, cell activation, growth, differentiation and proliferation. The SLIC-1 proteins provide novel diagnostic targets and therapeutic agents to control or modulate SLIC-1 molecule-associated disorders such as an inflammatory or immune
                                                                                                      Human; inflammatory bowel disease 1 protein, IBD1, IBD1prox, intestinal inflammatory disease; apoptosis, NF-kappa B, cancer; inflammatory disease; immune disease; cryptogenetic inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     glycoprotein ligand (PSGL-1) binding protein, useful as targets for developing modularing agents to regulate a variety of cellular processes including signal transduction -
                FR2806739-A1
                                                                                                                                                                                                                                03 JAN 2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           system disorder, a cardiovascular disorder, a cellular proliferation, activation, adhesion, growth, differentiation or migration disorder or
                                                                                                                                                                                       Amino acid sequence of IBD1prox protein.
                                                                                                                                                                                                                                                                       AAG79120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a haematopoietic or thrombotic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 14; Fig 1; 108pp; English.
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                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                        AAG79120 standard; Protein; 334 AA
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                                                                                         hemorrhagic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MASPEHPGSPGCMGPITQCTARTQQEAPATGPDLPHPGPDGHLDTHSGLSSNSSMTTREL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MASPEHPGSPGCMGPITQCTARTQQEAPATGPDLPHPGPDGHLDTHSGLSSNSSMTTREL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LDFLTRPELREAFGC1.RAGQYPRALELLLRVLPLQEKLTAHCPAAAVPALCAVLLCHRDL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRGITLKELTVREYLH 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UUYWUNUKCRWKHVKLLFEIASAPIEEPKVSKFVVYQIIVIQTGSFDNNKAVLERRYSDF 120
                                                                                                                                                                                                                                                                                                                                                                                                         PRGITLKELTVREYLH 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DRPAEAFAAGERALORLOAPEGHPYYAPLLDAMVPLAYALGKDFVTLOEPLEESQLERPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DRPAEAFAAGERALORIOAREGHRYYAPLLDAMVRLAYALGKDEVTLOERLEESOLRRPT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LDFLTRPELREAFGCLPAGQYPPALELLLPVLPLQEKLTAHCPNAAVPNLCAVLLCHRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AKLOKALLKTEREETEDVEEPRKHLTGNEAEEMICERRPALOEYLGLLYAIRCVRRSREF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             316;
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                                                                                                                                                                                                                              (first entry)
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                                                                                         Crohn's disease; Blau syndrome
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RESULT 3 AAB43067 ID AAB4

AAB43067 standard; Protein; 148

AAB43067

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source of (anti)sense oligonucleotides, for recombinant production of polypeptides, and in screening for interactive compounds. The polypeptides are used to raise specific antibodies which useful for diagnostic detection or purification of IBD1 and IBD1prox, to screen for specific binding agents, potential therapeutic agents. The IBD1 and IBD1prox polynucleotides and polypeptides are useful for treatment and prevention of inflammatory and/or immune diseases or cancer, where associated with mutations in genes corresponding to IRD1 and IRD1prox, especially cryptogenetic inflammation of the intestines (hemorihagic rectocolitis, Crohn's disease and Blau syndrome).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inflammatory disease. The IBD1 gene is probably involved in regulation of apoptosis and activation of NF-kappa B. The IBD1 and IBD1prox polynucleotides are is useful as source of probes and primers, as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents a human protein designated IBD1prox. The IBD1prox protein is in proximaty to a gene encoding inflammatory bowel disease 1 (IBD1) protein, which is associated with intestinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; Page 73-74; 97pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New human nucleic acids associated with intestinal inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AA165593, AA165594.
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                                                                                                                                                                                                                                                                                                                                                                                     1 MASPEHPGSPGCMGPITQCTARTQQEAPATGPDLPHPGPDGHLDTHSGLSSNSSMTTREL 60
                                                                                                                                                                                                                                                                                                         QQYWQNQKCRWKHVKLLFEIASARIEERKVSKFVVYQIIVIQTGSFDNNKAVLERRYSDF 120
PRGITLKELTVREYLH 316
                                                             DRPAKAFAAGERALQRLQAREGHRYYAPI.(DAMVRLAYALGKDFVTLQERLEESQLRRPT
                                                                                                                                                                                                  AKLQKALLKTFPEETEDVEFPPKHLTGNFAEEMTCEPPPALQEYLGLLYATPCVPRSPEF
                                                                                                                                                                                                                       AKLQKALLKTFPEE1EDVEFPPKHLTGNFAEEM1CEPPPAN.QFYLGLLYAIPCVPBSPEF
                                                                                                                                                                                                                                                                                                                                                                MASPEHPGSPGCMGPITQCTARTQQEAPATGPDI.PHPGPDGHLDTHSGLSSNSSMTTREL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001-608364/70
                                                                                                                      LDFLTRPELFEAFGCLRAGQYPRALELLLPVLPLQEKLTAHCPAAAVPALCAVLLCHRDL
                                                                                                                                                          LDFLTR PELREAFGCIRAGQYPPALELLIPVI.PI.QEKLTAHCPAAAVPALCAVLLCHKUL
                                                                                                                                                                                                                                                                                  QQYWQNQKCRWKHVKLLFETASARTEEPKVSKFVVYQTTVTQTGSFDNNKAVLERRYSDF
                                        DRPASAFAAGERALUPUJARSHHYYAPIIINAMVPLAYALGKUFVTLQERLEESQLERPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     useful for diagnosis, prognosis and control of these diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             334 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thomas G,
                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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100.0%, F
vative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1650; DB 22; Fied. No. 2.5e 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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0;

08-FEB-2001 (first entry)

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antipsoriatic; antiparkinsonian; nootropic; immunosuppressant; consteopathic; anticonvulsant; antiarthritic; immunosuppressant; cimmunostimulant; cardiant; thrombolytic; coagulant; vasctropic; cimmunostimulant; operative; dermatological; immunosuppressive; cantiinflammatory; antibacterial; antiviral; antifungal; antirheumatic; cantiinflammatory; antibacterial; antiviral; antifungal; antirheumatic; cantithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an OPFX-associated disorder The nucleic acids can be used to express OPFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritts, graft vs host disease, cardiovascular disease, diabetes mellitus, typertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, alleriae, aplastic anaemia, burns, wounds, borders, asthma, collerail or fungal infection, malaria, autoimmune disorders, asthma, collerail anaemia, burns, wounds, boat and cartilage damage, coagulation; to inhibit thrombosis; and as a contraceptive.
        Matches
                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel nucleic acids and peptides derived from open reading frame useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
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02-APR-1999; 99US-0127736.
05-APR-1999; 99US-0127728.
30-MAP-2000: 2000US-0540763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 11; Page 4838-4839; 5507pp; English.
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                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CURA-) CURAGEN CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal, antirheumatic; antithyroid;
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    Local Similarity hes 85; Conserv
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                                                                                                                                                                         148
        Conservative
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                                        , 25°56
18°56
18°56
1; Mismatches
                                        Score 464, DB 21,
Pred. No. 4 46-40;
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                                                                                Length 148;
Indels
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Gaps
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RESULT 4
AAM89008
AD AAM8
AC A
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14-AUG-2000
18-AUG-2000
22-AUG-2000
22-AUG-2000
23-AUG-2000
23-AUG-2000
30-AUG-2000
01-SEP-2000
01-SEP-2000
01-SEP-2000
05-SEP-2000
05-SEP-2000
06-SEP-2000
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14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
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19-MAY-2000;
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                                        expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynuclectides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynuclectides may be used to prevent, proteins and treat immune/haematopoletic-related discusses, especially cancers and cancer merastases of haematopoletic antigen genomic to AAK87694 represent human immune/haematopoletic antigen genomic
                                                                                                                                                                                                                    AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM93921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis are treatment of diseases associated with inappropriate (I) expression. For
Seduence
                                                                                                                                                                                                                                                                                                                       Claim 11; SEQ ID NO 16601; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                  Rucleic arids encoding human immane/humatopoletic antigen polyperilies, useful for preventing, diagnosing and/or treating cancers and
                              represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                       example, they may be used to treat disorders associated with decreased
                                                                                                                                                                                                                                                                                                                                                       metastasis
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Human cancer cell growth inhibitor related protein SEQ ID NO:

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                        30-MAR-2001; 2001WO-US08631
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                                                                                                                                                                                   Human; chromosome mapping; gene mapping; gene therapy; forensic food supplement; medical imaging; diagnostic; genetic disorder
                                                                                                                                                                                                                                                   Novel human diagnostic protein #27885.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human protein, and the polynucleotide that encodes it, useful for inhibiting cancer cell growth \,\, -
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CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC constitution of the constitution of the constitution of the constitution of (II). The CC constitution of the constitution of (II) and the sequence tags (II) is useful in gene therapy techniques (II) or to treat disease states involving CC (II). (II) is useful for generating antibodies against it, detecting or cc quantitating a polypeptide in tissue, as molecular weight markers and as CC a food supplement. (II) and its binding partners are useful in medical cimaging of sites expressing (II). (I) and (II) are useful for treating CC disgorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations CC responsible for genetic discreters or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC amino acid sequences. ABG00010-ABG30377 represent novel human CC diagnostic amino acid sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed CC specification, but was obtained in electronic format directly from WIPO at the printed content of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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23-AUG:2000; 2000US:0649167.
                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 20; SEQ ID No 58253; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAS92081.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drmanac RT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to isolated polynucleotide (I) and
350 MASPEHPGSPGCMGPITQCTARTQQEAPATGPDLPHPGPDGHLD
                                                                                                                                                                                                                                       Local Similarity
                                                                                             1 MASPEHPGSPGCMGPITQCTARTQQEAPATGPDLPHPGPDGHLD 44
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                                                                                                                                                                                                                                                                                                                                                                                      580 AA;
                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                             15.5%, Score 255, DB 22; 100.0%; Pred. No. 2.1e-17;
                                                                                                                                                                                           0, Mismatches
                                                                                                                                                                                                                                                                              Length 580;
                                                                                                                                                                                           Indels
                                                                                                                                                                                      Gaps
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AAM84390 standard; Protein; 93

0

AAM84390;

07-NOV-2001 (first entry)

Human immune/haematopoietic antigen SEQ ID NO:11983.

cytostatic; gene therapy; vaccine; metastasis Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;

Homo sapiens.

WO200157182-A2

09-AUG-2001

17-JAN-2001; 2001WO-US01354

31-JAN-2000; 2000US-0179065. 04-FEB-2000; 2000US-0180628.

JUN-2000 JUN-2000 JUN-2000 JUL-2000 JUL-2000 JUL-2000 JUL-2000

MAR MAR MAR APR APR JUN JUN

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-2000;

- 2000; - 2000; - 2000; - 2000; JUL

2000:

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                                                                                                                                                                                                   02.0CT 2000
13.0CT 2000
13.0CT 2000
13.0CT 2000
20.0CT 2000
20.0CT
          Mucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
                                                                              WPI; 2001-483426/52
M FSDB, AAK57171.
                                                                                                                                                                  (HUMA-) HUMAN
                                                                                                                                 CA,
                                                                                                                                 Barash SC,
                                                                                                                                                                                                     2000CUS
2000CUS
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0254097.
0259678.
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0256719
0251479
0251856
0251868
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                                                                                                                                                                    SCI INC
                                                                                                                                 Ruben SM
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2000IIIS -0184564 2000IIIS -018076 2000IIIS -0190076 2000IIIS -0190076 2000IIIS -0190076 2000IIIS -020561 2000IIIS -0216647 2000IIIS -0216647 2000IIIS -0216647 2000IIIS -0217496 2000IIIS -0217496 2000IIIS -022767 2000IIIS -0227767 2000IIIS -02277767 2000IIIS -0227777 2000IIIS -0227777 2000IIIS -0227777 2000II

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2000; 2000; 2000; 2000;

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-Aug. -Aug.

-2000; 2000; -2000; -2000;

- 2000; - 2000; - 2000; - 2000;

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RESULT 8
ABB59625
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Best Local
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            The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased
                                                                                                     Disclosure; SEQ ID NO 5667; 21pp + Sequence Listing; English
                                                                                                                                                     New isolated nucleic acid
genes from Drosophila and
                                                                                                                                                                           New isolated nucleic
                                                                                                                                                                                                              N-PSDB;
                                                                                                                                                                                                                             WPI; 2001-656860/75
                                                                                                                                                                                                                                                                Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                  23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                      23-MAR-2001; 2001WO US09231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster polypeptide SEQ ID NO 5667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB59625 standard; Protein; 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 11; SEQ ID NO 11983; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                   (PEKE ) PE CORP NY
                                                                                                                                          interactions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93 AA;
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                                                                                                                                                                                                                                                                                                                                  2000US-191637P
2000US-0614150
therapeutics and pharmaceutical
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                                                                                                                                                     detection reagent for detecting 1000 for elucidating cell signalling and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 249; DB 22;
; Pred No. 6.1e-18;
0; Mismatches 0;
                                                                                                                                                                                                                                                              Myers EW;
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                                                   The invention
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                          Human; chromosome mapping; gene mapping; gene therapy; forensi food supplement; medical imaging; diagnostic; genetic disorder
                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human diagnostic protein #23116.
                            Claim 20;
                                                      biodiversity
                                                                New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                          N-PSDB; AAS87312
                                                                                                                                                                                                                     31-MAR-2000, 2000US-0540217
23-AUG-2000, 2000US-0649167
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                                                                                                                                                                                            (HYSE-) HYSEQ INC.
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                                                                                                                                      2001-639362/73.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LRAGQYPRALELLLRVLPLQEKLTAHCPAAAVP-----ALCAV----LLCHRDLDRPA 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FPAKVLMGNFKSELIGERSAAFEAFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MPPDGEDVKIKPFVVYELTVKONGATEDTOPAKIEPPYTDFPFLYLGIKPOHPAEMANKY 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----EEPKVSKFVVVQIIVIQTGSF-DNNKAVLEPPYSDFAKLQKALLKTEPEETEDVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PGPD-ELDSPAIEAAALDIPPPESDKALOKGVWERATSAEYKPTTDGSTVLRFDILLAHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PGPDGHLDT----HSGLSSNSSMTTRELQQ-YWQN-QKCRWK-----HVKLLFEIASARI
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                                                                                                                                                                RT,
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                       SEQ ID No 53484, 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      295 AA;
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                                                                                                                                                                  Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----LPLYIPLLHTCAHLWWQRGQDQKPITDRLTD 267
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27.7%;
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7.1
7.3
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Pred. No. 1.4e-10;
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                                                                                                                                                                                                                                                                                                                                                                                            torensic;
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The invention relates to isolated polynucleotide (I) and

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RESULT 10
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Best Local :
                                                                                                                                                                                            Reuroprotective, cytostatic; dermatological; immunosuppressive; tumour; antiinflammatory; anti HIV; antibacterial; antiinflammatory; cancer; immuno system disorder; rheumatoid arthritis; inflammatory condition; organ transplant rejection; infection; hepatitis C; blood disorder; sickle cell anaemia; hyperproliferative disorder; Gaucher's disease; neurodegenerative disorder; Alzheimer's disease; parkinson's disoase; chromosomal abnormality; Down syndrome; ischaemia, renal disorder, cardiovascular; respiratory; wound healing; endocrine; Addison's disease; reproductive system; gastrointestinal; liver disorder; AIDS; acquired immune deficiency syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynuclectide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and to produce other types of data and an ino acid sequences. ABG0001n-ABG30077 represent novel human diagnostic amino acid sequences. ABG0001n-ABG30077 represent novel human acid sequences.
                 17 JAN 2001; 2001WO-11901112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polypeptide (II) sequences (I) is useful as hybridisation probes, polymerase chain reaction (PCP) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags
                                                                02 AUG-2001
                                                                                                             WO200154733-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07 NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel signal transduction pathway protein, Seq ID 1052
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Novel polypeptides useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cancers, immune
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Best Local
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                     Venter JC,
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                                                                                                                                                                                                                                                           Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                           Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster polypeptide SEQ ID NO 5778
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                                                        (PEKE ) PE CORP NY
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32.3%; Pred. No. 0.00071;
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                   Myers EW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; secreted protein; immunosuppressive, antiarthritic, antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; cancer; opthalmalogical; autoimmune disease; hyperproliferative disorder; cardiovascular disorder; cerebrovascular disorder; wound healing;
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WPI; 2000-611712/58
                                                            Rosen CA,
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17 DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nervous system disorder; aging; chemotaxis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                            (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  specification,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            143 KHLTGNF -- AEEMICEPPPALQEYLGILYAIPCVPPSPEFLDFLTPPE 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 TOORAPATGPOLPHPGPPGHLDTHSGLSSNSSMTTKELUUYWUNQKCRWKHVKLLFEIAS 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75 YGIVNRNGERYIVENIHMA-----GRQLCSRRYPEFANLHSLL----RKEFSGENFRK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ocal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001-656860/75.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                            Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   431 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                             9908-0172410.
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The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. AAC80522-CRNC30 and AAB45119 represent segmences
                                                                                                                                                                                                                                                                                                                                                          antirheumatic, antiproliferative, cytostatic, cardiant, vasotropic; cerebroprotective, nootropic; neuroprotective; antibacterial; virucide; fungicide; and opthalmalogical. The secreted proteins, polynucleotides, antagonists and agonists may be useful in treating, preventing and/or diagnosing diseases and disorders such as autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alternative polypeptides encoded by the genes, and amino acid sequences to which they are homologous. The genes and proteins have activities dependent on the tissues and cells in which they are expressed. Examples
Sequence
                                                                                                                                                                                                                                                                       system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal in
                                                                                                                                                                                                                                                                                                                                cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polynucleotide sequences AAC80531-C80580 represent cDNA encoding human secreted proteins AAB45120-B45169. Sequences AAB45170-B45225 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 28; 440pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAC80545.
                                                     the invention.
                                                                                used in the isolation and characterisation of the genes and proteins of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Parkinson's diseases and cancers -
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168 AA;
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                                                                                                                                                                                            Matches
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135 ESD 137
                            186 RPE 188
                                                                                         130 TERRETEDVEFORKHUTG----NEAEEMICERPRAIOEYLGULYAIPCVPPSPEFUDELT 185
                                                            79 --KREFANFTFPR--LPGKWPFSLSEQQLDARPRGLEEYLEKVCSIPVIGESDIMQEFLS 134
                                                                                                                             40
                                                                                                                                                        70 RWKHVKLLEEIASARIEEPKVSKEVVYQIIVIQTGSEDNNKAVLEPRYSDEAKLQKALLK 129
                                                                                                                                                                                                         Local Similarity
                                                                                                                         RYKHV-----EQNGEKFVVYNVYMA-----GPQLCSKPYPEFAILHQNL-- 78
                                                                                                                                                                                          Conservative
                                                                                                                                                                                                         28.5%;
                                                                                                                                                                                                                        6.8%;
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                                                                                                                                                                                                         Score 112.5, DB Pred. No. 0.0025
                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                        Indels
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ABB08158
                                                                                               hepatotropic, antiinflammatory, antipsoriatic, cytostatic, virucide; anticonvulsant; cerebroprotective; nootropic; neuroprotective; antiparkinsonian, transgenic, gene therapy.
                                          WO200242330 · A2
                                                                                                                                          Cytoskeleton-associated protein; CSAP; antiarteriosclerotic; human;
                                                                                                                                                                          Human cytoskeleton-associated protein (CSAP)-2 (ID: 959690CD1)
                                                                                                                                                                                                                                                                 ABB08158 standard; Protein; 541 AA
                                                                    Homo sapiens
                                                                                                                                                                                                       (first entry)
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30-MAY-2002

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Best Local
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08-NOV-2000;
07:DEC-2000;
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Arvizu C,
antiinflammatory; anti-HIV; antibacterial; antiinflammatory; cancer, immune system disorder; rheumatoid arthritis; inflammatory condition; organ transplant rejection; infection; hepatitis C; blood disorder; sickle cell anaemia; hyperproliferative disorder; Gaucher's disease; neurodegenerative disorder; Allheimer's disease; Parkinson's disease; chromesomal abnormality, Down syndrome, ischaemia; renal disorder; cardiovascular; respiratory; wound healing, endocrine, Addison's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and modulators are useful for diagnosing, treating or preventing disorders associated with aberrant expression of CSAP, where the disorders are selected from a cell proliferative disorders such as arteriosclerosis, cirrhosis, hepatitis, psoriasis, cancer, a viral infection such as those caused by adenoviruses, heresviruses, and retroviruses, and a neurological disorder such as epilepsy, stroke, Alzheimer's disease, Huntington's disease, dementia, and Parkinson's disease. The polymentides are also useful in a number of drug screening techniques, and to analyse the proteome of a tissue or cell type. The present sequence represents a human CSAP-2 polymeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to human cytoskeleton-associated proteins (CSAP) and encoding polynuclectides. The CSAP polypeptides can be expressed by standard recombinant methodology. The CSAP polynucleotides, polypeptides
                                                                                                                                           Neuroprotective; cytostatic; dermatological; immunosuppressive; tumour; antiinflammatory; anti-HIV; antibacterial; antiinflammatory; cancer,
                                                                                                                                                                                                           Novel signal transduction pathway protein, Seg ID 1046.
                                                                                                                                                                                                                                                             07-NOV-2001
                                                                                                                                                                                                                                                                                                                                                AAU17481 standard; Protein; 141 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human cytoskeleton-associated protein, useful in diagnosis, prevention or treatment of cell proliferative disorders, viral infections and neurological disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ABLKORKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   541 AA;
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1e H, Tang YT, Lal PG, Batra S,
Ramkumar J, Griffin JA, Gururaja
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Lu DAM, s
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Sanjanwala
           Addison's disease
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2000US-0184664.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to novel isolated polypeptides (I), and polymuclectides (II). (II) and the antibody to (I) are useful for diagnosing, preventing and treating diseases including immune system disorders (e.g. congenital and acquired immunodeficiencies, autoimmune disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disorders (e.g. glomerulonephritis), cardiovascular disorders (e.g. arrhythmia), respiratory disorders, dermatological disorders, in wound healing, epithelial cell proliferation, endocine disorders (e.g. Addison's disease), reproductive system disorders, gastrointestinal disorder (inflammatory disorders), liver disorders (cirliosis) as stimulators of B-cell responsiveness to pathogens, activators of T-cells, to induce higher affinity antibodies, and as a means to induce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disorders, primary haematopoletic disorders, hyperproliferative disorders (e.g. Gaucher's disease and cancer), neurodegenerative disorders (e.g. Alzheimer's disease, Parkinson's disease), chromosomal abnormalities (Down syndrome), ischaemic injury (e.g. stroke), renal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and other blood-related disorders (sickle cell anaemia), mycloproliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel polypeptides useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cancers, immune disorders and neuronal disorders -
                    WO200175067-A2
                                                                                                               Human, chromosome mapping, gene mapping, gene therapy, forensic;
                                                                                                                                                                 Novel human diagnostic protein #22886.
                                                                                                                                                                                                           18-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                              ABG22895 standard; Protein; 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tumour proliferation in pathologies e.g. acquired immune deficiency syndrome (AIDS). AAU17659 AAU17683 represent novel signal transduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transplant rejections and graft versus host disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WFI; 2001-465460/50
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                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pathway protein, amino acid sequences of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             128 LKTFREEIEDVEFPRKHLTGNFAEEMICERRRALQEYL 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 GPGSGGSPRVPDEAGAHFSPGTVPGFilsQTSEDQSL-----SDFEISNRALINVW---
                                                                                                  supplement, medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KCRWKHVKLLFEIASARIEERKVSKFVVYQIIVIQTGSFDNNKAVLERRYSDFAKLQKAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polypeptide (II) sequences. (I) is useful as hybridistation probes, (for polypeptide (II) sequences. (I) is useful as hybridistation probes, (for polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The complete are also used in diagnostics as expressed sequence tags (for identifying expressed genes. (I) is useful in gene therapy techniques (II) is useful for generating antibodies against it, detecting or (II). (II) is useful for generating antibodies against it, detecting or (quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating (disorders involving abstrant protein expression or biological activity. (The polypeptide and polynuclectide sequences have applications in (II) and (II) are useful for treations (II) and (II) are useful for treations (II) and (II) are useful for treations (II) are polypeptide and polynuclectide sequences have applications in (II) are polypeptide and polynuclectide sequences have applications in (II) and (III) are useful for treations (II) and (III) are useful for treations (II) and (III) are sequences. Abg000101-Abg30377 represent nowled human (II) and (III) are sequences and (II) are sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO (II) are useful format directly from WIPO (II) are useful format directly from WIPO (II) are useful format directly from WIPO (II) are polypeptide and po
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Matches 38; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drmanac RT, Liu C,
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23-AUG-2000, 2000US-0649167.
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                                                                                                                  137 F---RGGEVTRPLEVSRDLHILP 156
                                                                                                                                                                       193 FGCLRAGQYPRALELL--LRVLP 213
                                                                                                                                                                                                                                                                                             138 VE----FPRKHLTGNFAREMIC-EPPPALQEYLGLLYAIRCVRRSREFLDFLTRPELREA 192
                                                                                                                                                                                                                                    86 LEEFPAFPRAQVFGRFEASVDSPEPRKGAEDLLRFTVHIPALNNS------POLKEF 136
                                                                                                                                                                                                                                                                                                                                                         26 YTVSDPPTHPKGYTEYKVTAQFISKKDPEDVKEVVVWKPYSDFPKLHGDLAYTHPNLEPP 85
                                                                                                                                                                                                                                                                                                                                                                                                            78 FEIASARIEERKVSKFVVYQIIVIQTGSFDNNKAVLERRYSDFAKLQKALLKTFREEIED 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       166 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.5%; Score 107.5; DB 22; Length 26.6%; Pred. No. 0.0083; ative 24; Mismatches 62, Indels
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	Sequence 6, Appli	619	Sequence 28, Appl	Sequence 2, Appli		Sequence 11828, A	1)	~	Sequence 811, App	Sequence 2, Appli	Sequence 1051, Ap	Sequence 1003, Ap	Sequence 1182, Ap	Sequence 1035, Ap	Sequence 1046, Ap	Sequence 1052, Ap	Sequence 2, Appli	Description

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4.6	4.6	4.7	4.7	4.7	4.7	4.7	4.8	4.8	4.8	4.8	4.8	4.8	4.8	4.8	4.8	4.9	4.9	4.9		5.C				5.0	5.0
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Sequence 2, Appli	Sequence 3, Appli	Sequence 615, App	Sequence 2, Appli	Sequence 36, Appl	Sequence 33, Appl	Sequence 7, Appli	Sequence 38, Appl	Sequence 35, Appl	Sequence 39, Appl	Sequence 37, Appi	Sequence 34, Appl	Sequence 32, Appl	Sequence 30, Appl	Sequence 2, Appli	Sequence 6, Appli	Sequence 321, App	Sequence 2, Appli	Sequence 4, Appli	Sequence 2, Appli	Sequence 224, App	Sequence 9, Appli	Sequence 13, Appl	Sequence 1620, Ap	Sequence 7, Appli	Sequence 15, Appl

ALIGNMENTS

	QY Z41 DREABAFAAGERALQREQAREGHEYYAPILDAMVELAYALGRDEVTIQERLEESQLERET 300
	Db 181 LDFUTPPELREAFOCT.PAGQYPPALETTLEVTPT.QEKTTAHCENAAVPATCAVITCHPDL 240
	Qy 181 LDELTREELREARGCHAAGCYPRALECLLPVHPHQEKLTAHCPAAAVPALCAVLLCHREC 240
	Db 121 AKLQKALLKTEPEEIEDVEFPFKHUTGNFAEEMICEFFFALQEYLGLLYAIPCVPPSPEF 180
	Qy 101 AKIQKALLKTERESISDVEFFSKHLTGMEAESMIGESFSALGEYLGLLYAIRGVEFSKEF)40
	Db 61 QQYWQNQKCPWKHVKLLFEIASAPIEEPKVSKEVVYQIIVIQTGSEDNNKAVLEPPYSDF 120
	QY 61 QQYWQNQKQBWKHVKLLFEIASAPIEERKVSKFVVYQIIVIQTGSFDNNKAVLERRYSDF 120
	Db 1 MASFEHFGSFGCMGPITQCTARTQQEAPATGPDLPHPGPDGHLDTHSGLSSNSSMTTREL 60
	QY 1 MASPEHPGSPGCMGPITQCTARTQQEAPATGPDLFHPGPFGHTHTHSGLSSNSSMTTFEL 60
0	Query Match 100.0%; Score 1650; DB 10; Length 316; Best Local Similarity 100.0%; Pred. No. 5.8e-149; Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps
	ORGANISM: Homo sapiens S-09-816-697-2
	TYPE: PRT
	; SEQ ID NO 2
	; NUMBER OF SEQ ID NOS: 4 ; SOFTWARE: PatentIn Ver. 2.0
	PRIOR
	; PRIOR APPLICATION NUMBER: 60/192,104
	FILE REFERENCE: GEN-5380
	37717
	; GENERAL INFORMATION: ; APPLICANT: Lorenz, M., et al.
	; Sequence 2, Application US/09816697 ; Patent No. US20020037840A1
	RESULT 1 US-09-816-697-2

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RESULT 3
US 09 764 868-1046
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US-09-764-868-1052
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Patent No. US20020168711A1
                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 1046
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                                                                                                 Ouery Match 6.6%; Score 108.5; DB Hest Local Similarity 25.9%; Pred No 0.0081;
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ32
                                                                                                                                                                                                                                                                                                                                                                                                           Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 1510
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                                                                                                                                                                                                                   NAME/KEY: SITE LOCATION: (69)
                                                                                                                                                                                        OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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14 GPITOCTARTOQEA-----PATGP-DLPHPGPDGHLDTHSGLSSNSSMTTRELQQYWQNQ 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             y Match 7.2%; Score 118; DB 9; Length 173; local Similarity 32.3%; Prod. Mo. 0.0013; hes 40; Conservative 22; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71 EIPSKHVR-NWVPKVLEQRRQGLETYLQAV-----ILENEELPKLFLDFLNVRHLPSLPK 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 IPSFRYEESDLERGYTVFKIEVLMNG----PKHFVEKPYSEFHALHKKLKKC----IKTP 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80 JASARIEERKVSK-FVVYCIIVIQTGSFDNNKAVLERRYSDFAKLCKALLKTFREETEDV 138
                                                                          41; Conservative
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                                                                        21; Mismatches
                                                                                                               DB 9; Length 141;
                                                                        63; Indels 33; Gaps
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US-09-764-868-1182
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US-09-764-868-1035
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                                                                                                                                                               Query Match
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CURRENT FILING DATE: 2001-01-17
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Best Local :
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TITLE OF INVENTION. Rucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ32
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CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT FILING DATE: 2001-01-17
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NAME/KEY: SITE
LOCATION: (124)
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                                                     95 VYQIIVIQTGSFDNNKAVLEFFYSDFAKLQKALLKTFREEIEDVEFFRKHLTGNFAEEMI 154
                                                                                                       / Match
6 0%; Score 98 5; DB 9; Length 66;
Local Similarity 36.5%; Pred. No. 0.025;
les 23; Conservative 11; Mismatches 24; Indels
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7 LYTLTVIGPGPPDCOPAQISPRYSDFEPLHPNIOPOFPGPMAAISFPPKRL-----REIL 61
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SEQ ID NO 1003
LENGTH: 165
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CURRENT APPLICATION NUMBER: US/09/764,868
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TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (1) OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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NAME/KEY: SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Y Match 6.0%; Score 98.5; DB 9; Length 1
Local Similarity 42.1%; Pred. No. 0.09;
198 24; Conservative 10; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 RPYSRFREMHKT-LKLKYAELAALEFPPKKLFGNKDERVIAERRSHLEKYLRDFFSV 122
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13 PGSTXAMDPLPAAAVGAAAEAEADEEADPPASDLPTPQAIEPQAIVQQVPAPSRMQMPQG 72
                                                                                                                       Local Similarity
                                            7 PGSPGCMGPI------PQCTARTQQEAPATGPDLPHPG-------PDG 41
                                                                                                 44;
                                                                                                                                                                                                                                                                                                                                                                                        6)
                                                                                            Conservative 27; Mismatches
                                                                                                                     23.3%;
                                                                                                             Score 98; DB 9
Pred. No. 0.21;
                                                                                                                                      DB 9; Length 278;
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                                                                                              62, Indels
                                                                                            Gaps
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; Sequence 811, Application US/09764868 ; Patent No. US20020168711A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT232
CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT FILLING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 1510

US-09-764-868-811

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-957-837A-2
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SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 5.8%; Score 95.5; DI Best Local Similarity 22.7%; Pred. No. 9.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/957,837A CURRENT FILING DATE: 2001-09-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: LOUGHNEY ET AL TITLE OF INVENTION: ATR-2 CELL CYCLE CHECKPOINT FILE REFERENCE: 27866/37760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1711 GQQAESKQSKREMER------EITPSLFSSFVAEIKVNWFKNRDEMLVVLPKLD 1758
1974 ATEMTLQRY 1982
                                                                                                         1914 ATVALQYPKAIFQKHRIEQWKTWMEELICNTTVERCQELYRKYEMQYAPQPPPTVCQFIT
                                                                                                                                                                                                                                                                                                                                                                                                                                               1759 GSLDEYLS-LQEQLTDVEKLQGKLLEEIEFLEGAEGVDHPSHTLQHRYSEHTQLQTQQRA 1817
                                                                                                                                                                                                                                                                                                                                1818 VQEAIQV------KLNEFEQWIT--HYQAAFNNLEATQ----LASLLQEISTQMDLG- 1862
                                                                                                                                                              272 AMVRLAYALG-----KDFVTLQERL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    104 GSFDNNKAVLERRYSDFAKLQKALLK--TFREEIEDVEFPPKHLTGNFAFE-MICFPPPA 160
                                                 306 LKELTVREY 314
                                                                                                                                                                                                                                                                        221 HCPAAAVPALC-----AVLLCHRDLDRPAEAFAAGERALQPLQAREGHRYYAPILD 271
                                                                                                                                                                                                                                                                                                                                                                                       161 LQEYLGLLYAIRCVRPSPEFLDFLTPPEI.REAFGCUPAGGYPPALELLLFVI.PLGEKITA 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                164 ALKREVNLV 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     160 ALQEYLGLL 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100 VIQTGSFDNNKAVLERPYSDFAKLQKALLKTFPEEIEDVEFPPKHLTGNFAEEMICEPPP 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48 GLSSNSSMTTRELQQYWQNQKCRWKHVKLLFEIASARIEERKVSKF----VVYQIIVIQT 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73 NPLLLSHT-LQELLARDTVQVELIPEKKGLFLKHVE--YEVSSQRF------ 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42 H--LDTHSGLSSNSSMTTRELQQYWQNQKCRWKHVKLLFEIASARIEERKVSKFVVYQII 99
                                                                                                                                                                                                                --PPSYVPATAFLQNAGQAHLISQCEQ-LEGEVGALLQQRRSVLRGCLEQLHHY----- 1913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----KSSVYRRYNDFVVFQEMLLHKFPYRMVPAI,PPKRMI,GAD--REFIEAPRR 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                APPLICANT: Millennium Pharmaceuticals, Inc
APPLICANT: Meyers, Rachel
APPLICANT: Rudolph-Owen, Laura
APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Tsai, Fong Ying
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LENGTH: 276
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CURRENT FILING DATE: 2001 02-15
PRIOR APPLICATION NUMBER: 08/997,212
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APPLICANT: Cheng Zou
TITLE OF INVENTION: 13277, 18480, 2245 OR 16228 NOVEL HUMAN TITLE OF INVENTION: PROTEIN KINASE MOLECULES AND USES THEREFOR FILE REPERRENCE: 38155-20020.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 1997-12-23
PRIOR APPLICATION NUMBER: 60/051,446
PRIOR FILING DATE: 1997-07-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: SERINE/7
FILE REFERENCE: GH-70124-C1
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LOCATION: (223)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                   140 FPRKHLTG NFAEEMICERRRALQEYL 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          140 FPRKHLTG-NFAEEMICERRRALQEYL 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           y Match 5.7%; Score 93.5; DB 10; Length 496; Lecal Similarity 31.0%; Pred No. 1 %;
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                                                                                                                                                                                                                                                                                                                                                                        72 IPAKRIFGDNEDPDFIKOPPAGLNEFI 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 IPAKPIFGDNEDPDFIKORPAGLNEFI 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18 IPSSDEHREKKKPFTVYKVLV----SVGRSEWFVFRRYAEFDKLYNTLKKOF--PAMALK 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80 IASAPIEEPKVSKEVVYQIIVIQTGSEDNNKAVLERPYSDEAKLQKALLKTEPEEIEDVE 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 IPSSDEHREKKKPFTVYKVI.V----SVGRSEWFVFRRYAEFDKLYNTLKKOF PAMALK 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80 JASARIEERKVSKEVVYQIIVIQTGSFDNNKAVLERRYSDFAKLQKALLKTFREEIEDVE 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27;
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                                                                                                                                                                     US-09-815 242 11828
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CUPPENT FILING DATE: 2001 03-21
PRIOP APPLICATION UNMBER: 60/191,078
PRIOP FILING DATE: 2000-03-21
PRIOP FILING DATE: 2000-03-21
PRIOP FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
FRIOR APPLICATION NUMBER: 60/207,727
FRIOR APPLICATION NUMBER: 60/207,727
FRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
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                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000 11-27
PRIOR AFPLICATION NUMBER: 60/257,931
PRICH FILING CATE: 2000 12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001 02-16
NUMBER OF SEQ ID NOS: 14110
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                                                                                                                                                                                                                                                                              SEQ ID NO 11828
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL
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                                                          Matches
                                                                                       Best
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                                                                                                           Query Match
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PPIOP APPLICATION NUMBER: US 60/219,028
PPIOP FILING DATE: 2000-07-18
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CURRENT FILING DATE: 2001-07-18
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TITLE OF INVENTION. Identification of Essential Genes in
TITLE OF INVENTION. Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-815-242-11828
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ORGANISM: Homo sapiens
                                                                                                                                                                                          ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                    LENGTH: 1162
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  106 FONNKAVLEPRYSDFAKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  y Match 5.6%; Score 92 %; DR 10; Length 1066;
Local Similarity 26.9%; Pred No. 4.6; Indels 7; Gaps
hes 28; Conservative 21; Mismatches 48; Indels 7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87 ERFVSFFVVYQT IVIQTGSELMNKAVLERKYSDEAKLQKALLKTERBEIEDVE--- 139
                                                                              Match 5.4%; Score 89; DB 10; Length 1162; Local Similarity 23.6%; Pred. No. 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION:
                                                          60;
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Zyskind, Judith W.
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                                                          Conservative
                                                       30;
                                                       Mismatches 80; Indels
QKALL----KTEFEEIEDVEF-----PFKHL- 145
                                                    84; Gaps
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PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05:-23

PRIOR FILING DATE: 2000-05:-26

PRIOR PRILING DATE: 2000-05:-26

PRIOR PRILING DATE: 2000-05:-26

PRIOR PRILING DATE: 2000-10:-23

PRIOR PRILING DATE: 2000-10:-23

PRIOR PRILING DATE: 2000-10:-23

PRIOR PRILING DATE: 2000-10:-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR APPLICATION NUMBER: 60/259,308

PRIOR PRILING DATE: 2001-02:-16

PRIOR PRILING DATE: 2001-02:-16

PRIOR PRILING DATE: 2001-03:-16

PRIOR PRILING DATE: 2001-03:-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 10617
                                                                                                                                                                                                                                                                                                                  Matches 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10617, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 14110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/191,078
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: ELITRA.011A
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                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENGTH: 1045
546 ELTEVEKTVORFTETLSALGAEKOOKE-----SQLOEQ----EAAYTEEQEQLAAQFA 594
                                                   153 MICEPRPALQEYLGLIYAIPCVRPSPEFLDFLTRPELPEAFGCLPAGQYPPALELLLPVL 212
                                                                                                                                                      106 FDNNKAVLERRYSDFAKLQKALLKTFREEIE-----DVEFPRKHLTGNF------AEE 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 285 VTLQERLEESOLRR 298
                                                                                                                                                                                                                                                      48 GLSSNSSMTTREL'ΩΩΥΜΩΝΩΚΌΡΗ-ΚΉΥΚΙΤΕΕΙΑSARIEEPKVS-ΚΡΎΥΥΩΙΙVΙÇTGS 105
                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                         GTLEKANFECSSVADHWCMFVERWCKNCKAWQKISQNQVELHELTQRFAVEQ----QQKS 487
                                                                                                      AE--EAKLQTKKSQWASLQIQRLSLLLEEGEPCPVCGSLEHPKQQTHQEVSLEEIDQAER 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PA-----EAFAAGER----ALQRLQAREGHRYYAPLLDAMVRLAYALGKDF 284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T--DLREELG------PQLEPLHPQAQSAEKYQEH--KAEERQLKAQLGAVRWRDLNE 242
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Zyskind, Judith W.
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                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                         %; Score 88; DB 10; Length 10;
%; Pred. No. 12;
57; Mismatches 128; Indels
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Sequence 28, Application U; Patent No. US20220123082A1
GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: US 60/304,101
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: to be assigned
PRIOR FILING DATE: 2001-10-22
PRIOR FILING DATE: 2001-10-22
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CURRENT APPLICATION NUMBER: US/10/098,979
CURRENT FILING DATE: 2002-03-14
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APPLICANT: Cimbora, Daniel
TITLE OF INVENTION: TSG101-INTERACTING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
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NUMBER OF SEQ ID NOS: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     595
                                                                                                                                                                      577 -----SHSSDLSTIQERMEE 591
                                                                                                                                                                                                                     272 AMVRIAYALGKDFVTLQERLEE 293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             292 VSSIVMSTLRELGQTWANLDHMVGQLKILLKSVLDQWSSHKVAFDKINSYLMEARYSLSR 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49 LSSNSSMTTRELQQYWQNQK------CRWKHVKLLFE-IASARIEER-KVSK 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                             KDIADDEVATWIQDCNDLLKGLGTVK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                    VNMRWNNLLEEIAEQL--QSSKALLQLWQRYKD--YSKQCASTVQQQEDRTNELLKAATN 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VEFPRKHLTGNFAEEMICERRRAL----QEYLGLLYAIRCVP-----PSPEFLDFLTP 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FVV----YQIIVIQTGSFDNNKAVL---ERRYSDFAKLQKALLK-----TFREEIED 137
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                                                                                                                                                                                                                                                               SDQLSLSQHLCALEQALCKQQTSLQAGVLDYETFAKSLEALEAWIVEAEEILQGQDP----
                                                                                                                                                                                                                                                                                                         ------LCAV--LLCHRDLDRPA-----EAFAAGERALQR--LQAREGHRYYAPLLD 271
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                                               Application US/10042417
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                                                                                                                                                                                                                                                                                                                                                                                                     ---ELREAFGCLRAGQYPRALELLLRVLPLQEKLTAHCPAAAVPA-- 229
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22.4%; Pred. No. 33;
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                                                                                                                                                                                                                                                                                                                                                        --DSLFFLHELGEQLKQQVDASAASAIQ 519
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TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF

APPLICANT: Pagano, M.

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; TITLE OF INVENTION: PROLIFERATIVE AND DIFFERENTIATIVE DISORDERS; FILE REFEBENCE: 5914-090-999; CURRENT EXPLICATION NUMBER: US/10/042,417; CURRENT EVILING DATE: 2002-01-07; PRIOR APPLICATION NUMBER: 50/260,179; PRIOR FILLING DATE: 2001-01-5; NUMBER OF SEQ ID NOS: 89; SOFTWARE: Patentin Ver: 2.0; SEQ ID NO 28; LENGTH: 621; TYPE: PRT
; ORGANISM: Homo sapiens
US 10-042 417-28
Smarch completed: April 20, 2003, 14-12-15 dob-time : 44 secs
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                                                                                                         255 IELQSQ··----VLDAMNYVLY 270
                                                                                                                                                                                                             205 YCNPLSDISLKDIQAQID-----SIVELVCKTL---PGINSPHPSLAFKAGESSMIME 254
                                                                                                                                                                                                                                                                   201 YPRAL-ELLLRVLPLQEKLTAHCPAAAVPALCAVLLCHRDLD--RPAEAFAAGERAL--- 254
                                                                                                                                                                                                                                                                                                                    145 EDELUCILNMEGEKALTWKYYAKFILYYLPQQKILNNLKAFLQQDDDYESYLEGAVYIDQ 204
                                                                                                                                                                                                                                                                                                                                                                       150 AEEMIC----EPPPALQ-EYLG--LLYAIPCVPPSREFLDFLTBPELREAF--GCLRAGQ 200
                                                                                                                                                                                                                                                                                                                                                                                                                              103 ------ROKAGLEAR-----KIVASFSKRFFSEHVPCNGFSDIENLEGPEIF----F 144
                                                                                                                                                             255 ORLOAREGHRYYAPILDAMVRLAY 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48 GLSSNSSMTTRELQQ-----YWQNQ-KCRW-----KHVKLLFEIASARIEERKYSKFVVYQI 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99 IVIQTGSFDNNKAVLERRYSDFAKLQKALLKTFREE------IEDVEFPRKHLTGNF 149
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Result
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Maximum DB seq length: 200000000
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2: /cgn2_6/ptodata/1/iaa/5B_CCMB.pcp:*
3: /cgn2_6/ptodata/1/iaa/6B_CCMB.pcp:*
4: /cgn2_6/ptodata/1/iaa/6B_CCMB.pcp:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_CCMB.pcp:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pcp:*
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                  Copyright (c) 1993 - 2003 Compugen Ltd.
        US-09-906-865-4
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US-09-8-625-322-2
US-08-821-352A-8
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Query Match 6.0%; Scott 49 %; PR 3; Let Best Local Similarity 25.0%, Fred. No. 0.031;	US-08-96-865-4 US-08-96-865-4 Sequence 4, Application US/08906865 Patent No. 6040168 GENERAL INFORMATION: APPLICANT: Greengard, Paul AFFLICANT: Kao, Hung-Teh ITILE OF INVENTION: AND USES THERBOF INVESSEE: David A. Jackson, Esq. STREET: \$10or CITY: Hackensack Ave, Continental Plaza, 4t STREET: Floor CITY: Hackensack Ave, Continental Plaza, 4t STREET: Hoor CITY: Hackensack Ave, Continental Plaza, 4t STREET: Hoor CITY: Hackensack Ave, Continental Plaza, 4t STREET: Ploor CONUTRY: USA ZIP: 07601 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER READABLE FORM: MEDIUM TYPE: PATENTIN Release #1.0, Version #1.30 CURRENT AFFLICATION INTERACTION: AFFLICATION HUMBER: US/08/906,865 FILING DATE. AFFLICATION HUMBER: US/08/906,865 FILING DATE. AFFLICATION HUMBER: 536 ATTORNEY/AASHT INFORMATION: TELEFIONE: 201-487-5800 TELEFAX: 201-343-1664 STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein DESCRIPTION: /desc = "Synapsin Ia" HYPOTHETICAL: NO CRIGINAL SOURCE: CRAANISM. Homo sapiens	28 78.5 4.8 706 2 US-08-689-276A-4 29 78 4.7 993 4 US-09-060-410-4 30 78 4.7 3111 2 US-08-460-309-4 31 78 4.7 3111 2 US-08-125-077-4 32 76.5 4.6 557 4 US-09-271-815-2 33 76.5 4.6 2101 1 US-08-470-950-4 35 76.5 4.6 2101 1 US-08-467-781-4 36 76.5 4.6 2101 1 US-08-467-781-4 37 76.5 4.6 2101 1 US-08-467-781-4 38 76.5 4.6 2101 2 US-08-195-487-4 39 76.5 4.6 2101 2 US-08-195-487-4 30 76.5 4.6 2101 2 US-08-195-487-4 41 76 4.6 2101 2 US-08-195-487-4 42 76 4.6 2101 2 US-08-195-487-4 43 76 4.6 2101 2 US-08-764-870-5 42 76 4.6 454 4 US-09-390-117-5 43 76 4.6 454 6 US-09-390-117-5 44 76 4.6 2639 4 US-09-390-383-3 45 75.5 4.6 204 1 US-08-419-414-9
Length 696;	TI GENE	Sequence 4, Appli Sequence 4, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 6, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 6, Appli Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli

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RESULT 3 • US-09 417-822-2
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EARLIER FILING DATE: 1997-09-06
NUMBER OF SEQ ID NOS: 8
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FILE REFERENCE: 600-1-202 OF
CURRENT APPLICATION NUMBER: UC/09/129,668B
CURRENT FILING DATE: 1998-08-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Kao, Hung Teh
TITLE OF INVENTION: DNA ENCODING THE HUMAN SYNAPSIN III GENE AND USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Greengard, Paul APPLICANT: Porton, Barbara
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                                                                                                                                                                                                                                                 165 IGILLYAIRCVRRSREFI.DF-LTRPELREAFGCLRAGQYPRALELLLRVLPLQEKLTAHCR 223
                                                                                                                                                                                                                                                                                                    119 IDEPHTDWAKYEKG--KKTHGEIDIKVEQAEFSDLNLVAHANGGFSVDMEVLRN----- 170
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                                                                                                                                               224 AAAVEALCAVILICHEDIDEFAFAFAAGERALQRIQAPEGHPYTAFILD 271
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TITLE OF INVENTION: ATR-2
FILE REFERENCE: 27866/35633
CURRENT AFPLICATION NUMBER US/00
CURRENT FILING DATE: 1999-10-14
NUMBER OF SEC ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
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LENGTH: 2930
SEQ ID NO 93
LENGTH: 3072
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APPLICANT: Bristol-Myers Squibb, Co.
APPLICANT: Beyer, Stefan
APPLICANT: Beyer, Stefan
APPLICANT: Bereker, Helmut
APPLICANT: Brandt, Petra
APPLICANT: Cino, Paul M
APPLICANT: Conderry, Brian A
APPLICANT: Goldberg, Steven L
APPLICANT: Goldberg, Steven L
APPLICANT: Hofle, Gerhard
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 93, Application US/09413814
                                                                              CURRENT APPLICATION NUMBER: US/09/413,814
CURRENT FILING DATE: 1999-10-07
LAFGLER AFFLICATION NUMBER: DE 190 4C 473.2
EARLIER FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 107
                                                                                                                                                                                                                     TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide TITLE OF INVENTION, heteropolyketide compounds FILE REFERENCE: PCT/US 99/23535
                                                                                                                                                                                                                                                                                                                APPLICANT: Mueller, Joachim APPLICANT: Reichenbach, Hans
                                                         SOFTWARE: Patentin Ver.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         161 LQEYLGLLYAIRCVPRSPEFLDFLTPPELPEAFGOLPAGQYPPALEILLPVLPLQFKLTA 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     104 GSFUNNKAVLERRYSDFAKLOKALLK--TERRETEDVEFPRKHLTGNFAEE-MICERRPA 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48 GLSENSSMTTRELQQYWQNQKCKWKHVKLLFEIASARIEERKVSKF----VVYQIIVIQT 103
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                                                                                                                                                                                                                                                                                US-09-413-814-80
                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide
TITLE OF INVENTION: heteropolyketide compounds
FILE REFERENCE: porJus 99/23535
CURRENT APPLICATION NUMBER: US/09/413,814
CUPPENT FILING DATE: 1999-10-07
EAPLIER APPLICATION NUMBER: US/09/413,814
CUPPENT FILING DATE: 1999-10-07
EAPLIER FILING DATE: 1999-10-09
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 80
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Parent No 6225064
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                                                                                                                                                                               Matches
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APPLICANT: Goldberg, Steven L
APPLICANT: Hofle, Gerhard
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                                                                                                                                                                                                                                                                                             LENGTH: 3079
TYPE: PRT
ORGANISM: Sorangium cellulosum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         934 PEFPFALTEGOPAMW---
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                                                                      896 EHPTLAQLASHLSSGAAS--TSAAAATALERGLTRPD------GPSSPRVAT 939
S7 TPELOOYWONOKOPWKHVKLLFELASARIEERKVSKFVVYQI-IVIOTGSFDNNKAVLER 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57 TRELOGYWONOYCHWHYVII.FETASABIEEBYVSYFVVYQI-IVIQTGSFDHHXAVLER 115
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                                                                                                                      5 EHPG-----SPGCMGPITQCTARTQQEAPATGPDLPHPGPDGHLDTHSGLSSNSSMT 56
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                                                                                                                                                                            Conservative
                                                                                                                                                                    5.5%; Score 90; DB 4; Length 3079,
21 1%; Fred Nc 3 7,
tive 34; Mismatches 126; Indels 120; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---FVTLQERLEESQLRRPTFRGITL 306
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                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO. 3
SEQUENCE CHARACTERISTICS.
LENGTH: 522 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWAPE: Petentin Pelease #1.0, Version #1.25
CUPPENT APPLICATION DATA:
APPLICATION NUMBER: US/08/625,322
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APPLICANT: Cadena, Deborah L.
TITLE OF INVENTION. Sorting Nexins and Methods of Using Same
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1046 DIERGPLIRVHVWRRGEGOPPLLTVVVHHLVVDYWSFALLVRELGELYSALRAGRPPO-- 1103
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149 FAESMICEPERALQETUGLIYAIFOVEFSFEFLDELIFFFELFEAFGOLF - AJ
                                      174 PLEPSKQFAVKPPFSDFLGLYEKL----SEKHSQNGFTVPPPPEKSLIGMTKVKVGKEDS
                                                                                    105 -SFDNNKAVLEPPYSDFAKLQKALLKTFPEEIEDVEF----PRKHLTG------N 148
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                    TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Campbell, Cat
REGISTRATION NUMBER:
                                                                                                                                                                   50 SSNSSMTTREUGETWENGETOPWEHVELLELASAPIEEPEV----SKEVVYGIIVIGIG- 104
                                                                                                                                                                                                                                   Match 5.2%, Gcore 85.5, DB 1, Local Similarity 21 6%; Pred No. 0 76;
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4370 La Jolla Village Drive, Suite 700
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N: 435
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VI 1.2
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                                                                                                                                                                                                                                                                                      RESULT 8
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US:08 890-719-12
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APPLICANT: Hacon, Larry D
APPLICANT: Hunc, Henry D
APPLICANT: Fulton, Janet
TITLE OF INVENTION: Freduction of Antisera Specific to Major
TITLE OF INVENTION: Histocompatibility Complex Molecules in C
FILE REFERENCE: Dkt 0064.96 - Larry D. Bacon et al.
CURRENT FILING DATE: 1997-07-09
EARLIER APPLICATION NUMBER: 05/021,685
                                                                                                                                                                                                                 Sequence 8, Application US/08821355A Patent No. 5851775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12, Application US/08890719A Patent No. 6075125
                                                                                                                                                                                                              Patent No.
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                                                                                                                                                                                        GENERAL INFORMATION:
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                      APPLICANT:
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                                                                                                                                                             APPLICANT:
TITLE OF INVENTION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          410 FDÜRMKTWÖPWÖDAQATLOKKREAEARL 437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        y Match
5.2%; Score 85; DB 3; Length 338
Local Similarity 24.7%; Pred. No. 0.44;
hes 54; Conservative 24; Mismatches 67, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68 OTSOKSBOILFERINGELEPRYNGEGISSHTVDWMYGCDILEDGTIRGYRQYAYDGRDFIAF 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19 PGPGQPWFVDVGYVDGELFTHYNSTARRAVPRTEWIAANTDQQYWDSE------T 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80 IASARIEERKVSKFVVYQIIVIQTGSFDNNK-----AVLE-----PPYS----DFAKL 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------DGHLDTHSGLSSNSSMTTREL-----QQYWQNQKCRWKHVKLLFE 79
                 Vogelstein, Bert
Sparks, Andrew
                                                               Kinzler, Kenneth
                                                                                             Morin, Patrice
                                                                                                                 Clevers, Hans
Korinek, Vladimir
                                                                                                                                                               Barker, Nick
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Beta Catenin, TCF-4, and APC
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TELEFAX: 202-508-9299
TELEX: 97430 BMB UT
INFORMATION FOR SEQ ID NO:
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PEGISTAN NUMBER: 32,145
PEFERENTATION NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
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STREET: LVV.
CITY: Washington
TATE: DC
TATE: TCA
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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OPERATING SYSTEM: DOS
SOFTWARE. PASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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NUMBER OF SEQUENCES. 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd
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445 RHLHPQVSPLLSA 457
                                       260 REGHRYYAPLIDA 272
                                                                                 400 ---- EKAAAPAPFLPMTVLAAPGPQLPRTHPHTICCP-----
                                                                                                                       211 VEPLOEKETAHCPAAAVPALCA------VILICHPPLEFFAEAFANGERALCFECA 259
                                                                                                                                                                                                                                                   316 KVÍAECTLKESAAINQILGPRWHALGE
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                                                                                                                                                                   355 ERQLHMQLYPG--WSAPINYGKKKPESEEKHQESTTGGKKNAF--
                                                                                                                                                                                                                                                                                                                                       268 PPSG--KQELQFFBRNLFTQ------
                                                                                                                                                                                                    156 ERRPALQEYLGLLYAIP-----VVRPSPFFFLDFLTRPELFEAFGCLPAGQYPRALELLLE 210
                                                                                                                                                                                                                                                                                             99 IVIQTGSFDNNKA---VLEPPYSDFAKLQKALLKTFPEEIEDVEFPPKHLTGNEAEEMIC 155
                                                                                                                                                                                                                                                                                                                                                                            51 SNSSMTTRELQQYWQNQKCPWKHVKLLFEIASARIE-----ERKVSKEVVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
Wes 69; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
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                                                                                 -ASPQNCLLALRS 444
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; Sequence 8, Application US/09003687A ; Patent No. 5998600 ; GENERAL INFORMATION:

APPLICANT:

US-09-003-687A-8

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TITLE OF INVENTION: Beta Catenin, TCF-4, and A
TITLE OF INVENTION: Interact to Prevent Cancer
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
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APPLICANT:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION
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445 RHLHPQVSPLLSA 457
                                    260 REGHRYYAPLLDA 272
                                                                                                      211 VLPLQEKLTAHCPAAAVPALCA------VLLCHPDLDPPAEAFAAGEPALQPLQA 259
                                                                                                                                                                                                                116 KVIAECTUKESAAINQILGPPWHAUSP-----EEQAKYYELARK-------
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CITY: Washington
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                                                                                                                                                                                                                                                                                                                         51 SNSSMTTPELQQYWQNQKCPWKHVKLLFEIASARIE-----ERKVSKFVVY----QI 98
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                                                                     ----EKAAAPAPFLPMTVLAAPGPQLPRTHPHTICCP-----ASPQNCLLALRS 444
                                                                                                                                         EPQLHMQLYPG--WSAPDNYGKKKPPSPEKHQESTTGGKPNAF-----GTYP-----
                                                                                                                                                                            ERRRALQEYIGILYAIR-----CVRRSREFLDFLTRPELREAFGCLRAGQYPRALELLLR 210
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97430 BMB UT
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1001 G Street, N.W.
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Korinek, Vladimir
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E: No. 5998600e
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22.0%; Fred. No. 1;
ative 35; Mismatches 95; Indels 114, Gaps
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APPLICANT: Gill, Gordon N.
APPLICANT: Kurten, Richard C.
APPLICANT: Cadena, Deborah L.
TITLE OF INVENTION: Sorting N
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EARLIER APPLICATION NUMBER: 08/821,355
EARLIER FILING DATE: 1997-03-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Beta Catenin, TCF-4, and APC Interact to TITLE OF INVENTION: Prevent Cancer FILE REFERENCE: 1107.75741
CURRENT APPLICATION NUMBER: US/09/136,605A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: He, Tong-Chuan
APPLICANT: Kinzler, Kenneth
APPLICANT: Vogelstein, Bert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 28
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EARLIER FILING DATE: 1998-01-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 486
COMPUTER READABLE FORM:
                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        445 RHLHPQVSPLLSA 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             316 KVIAECTLKESAAINQILGPPWHALSP-----EEQAKYYELAPK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   260 REGHRYYAPLIDA 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    400 ----EKAAAPAPFLPMTVLAAPGPQLPRTHPHTICCP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                211 VLPLQEKLTAHCPAAAVPALCA------VLLCHRDLURPAEAFAAGERALQRLQA 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   355 ERQLHMQLYPG--WSARDNYGKKKPPSPEKHQESTTGGKPNAF-----GTYP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            156 ERRRALGEYLGLLYAIR-----CVFFSPEFLDFLTPPELPEAFGCLRAGQYPRALELLLR 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 268 PPSG--KQELQPFDPNLKTQ------AESKAFKFAKKPTIKKPLNAFMLYMKEMPA 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              215 PLYFLSP-----SCGYRQHFFAPTAAFGAFYFRFTHPSLMLGSGVFGHFAAIFHFAIV 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Y Match 5.1%, Score 84; D Local Similarity 22.0%, Pred. No. 1;
                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 SNSSMTTRELÖÖYMÖNÖKORWKHVKLLFEIASARIE-----ERKVSKFVVY----QI 98
                                                                                         CITY: San Diego
                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99 IVIQTGSFDNNKA---VLERPYSDFAKLQKALLKTFREEIEDVEFPRKHLTGNFAEEMIC 155
                         ZIP:
                                                                                                                                             ADDRESSEE:
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                         92122
                                                                     California
                                                                                                                E: Campbell and Flores
4370 La Jolla Village Drive,
                                           USA
                                                                                                                                                                                                             Sorting Nexins and Methods of Using Same
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                                                                                                                                                                                                                                                                                                                                      8 08-622-353-7
8 08-622-353-7
8 Sequence 7, Application US/08622353
Patent No. 5700925
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                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Bishai,
APPLICANT: Young,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acids
TOPOLOGY: line
WOLECHE
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                         NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE: 01-APR-199
CLASSIFICATION: 435
                                                                                                                                                                                                        APPLICANT: Demaio, James
TITLE OF INVENTION: A STATIONARY PHASE, STRESS RESPONSE
TITLE OF INVENTION: SIGMA FACTOR FROM MYCOPACTERIUM TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
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REFERENCE/DOCKET NUMBER: P-UD 1955
TELECOMMUNICATION NEORMATION
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NAME: Campbell, Cathryn A
REGISTRATION NUMBER: 31,8
                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183 TLLQDPDLRQ---FLESSELPRAVNTQALSGAGILRMVNKAADAVNKMTIKMNESDAWFE 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             132 HVVIEVATSSRKSIVGMTKVKVGKEDSSSTEFVEKRRAALERYL....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       295 QL 296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     251 ERALQRL ------OAPEGHRYYAPLLDAMVRLAYALGKDF---VTLQERLEES 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 DELTEPELREAFGCLRAGQYPPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               353 QI 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 EKÇÖÇKENLIYÇELKELHVSVEA - --- LVCHRKELSANTAAFAKSAAMLGNSEDHTÁL 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            y Match
4.9%; Score 81.5; DB 1; Length 451;
Local Similarity 19.9%; Pred. No. 1.7;
hes 60; Conservative 45; Mismatches 96, Indels 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
                                                                                    STATE:
                                                                                                                         STREET:
                                                               COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77 LFEIASARIEERKV----SKFVVYQIIVIQTGSFDMNKAVLERPYSDFAKIQKALLKTFP 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
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                                                                                                      Z
                                                                              Washington DC
                                                                                                                     1001 G Street, eleventh floor
                                                                                                                                                                                                                                                                     Young, Douglas B.
Zhang, Ying
                                                               USA
                                                                                                                                                                                                                                                                                                        Bishai, William R.
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Floppy disk
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RESULT 13
US:08 622 352A-9
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                                                                                                                                                                                                                                                                                                                                    Sequence 9, Application US/08622352A Patent No. 5824546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
4.3%; Scote 81, DB 1, Length 487;
Best Local Similarity 21.2%; Pred. No. 0.97;
Whiches F6. Conservative 38, Mismatches 108, Indels 109,
                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Bishai, Willis
APPLICANT: Demaio, James
TITLE OF INVENTION: PROJU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 7:
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 287 amino acids
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWAPE: Patentin Polease #; o, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 31 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     246 LRYYSNLTQSQI 257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              164 RSPTTAEIAERLRITEEEV-----LSCIEAGRSY------HATSLEAAGEGDGLP 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151 EE----MICERPRALQEYL/TLLYAIR/TVRPSREFL/FEL/TRPEL/KEAFG/CLKA/GQYPKALL 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107 FDPERGV---QFPTFAMPTVVGEIKRYFRDNVRTVHVFRRLHELWVQVNSATEDLTTAFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              106 FDNNKAVLEPPYSDFA--KLQKALLKTFREEIEDVEFPRK------HLTGNFA 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 202-508-9299
THI TERAX: 202-508-9299
                                                ZIP:
                                                                   COUNTRY:
                                                                                            STATE:
                                                                                                               CITY: Washington
                                                                                                                                   STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Streptomyces coelicolor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE
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                                                20005-3918
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                                                                                          DG
                                                                                                                               E: Pillsbury Madison & Sutro, L.L P. 1100 New York Avenue, N.W.
                                                                     USA
                                                                                                                                                                                                                                                                                          Bishai, William R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       202-508-9100
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                                                                                                                                                                                                                         PROM MYCORACTERIUM TUREFCULOSIS
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RESULT 14
US-08-826-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9, Application US/08826390
                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -08-826-390-9
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INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL: NO ORIGINAL SOURCE: ORGANISM: Stre
                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                         APPLICANT: DeMaio, James
TITLE OF INVENTION: Stationary Phase, Stress Response
TITLE OF INVENTION: Sigma Factor From Mycobacterium tuberculosis, and
TITLE OF INVENTION: Regulation Thereof
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Word Perfect CURRENT APPLICATION DATA:
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LENGTH: 287 amino acids
                                 COMPUTER READARLE FORM.

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               106 FONNKAVLERPYSOFA--KLOKALLKTFREEIEDVEEPRK-------HLTGNFA 150
                                                                                                                                   STATE: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    246 LRYYSNLTQSQI 257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    207 LLLPVI.PI.QEKLTAHCPAAAVPALCAVILLCHPDLDPPAEAFAAGEPALQRLQAREGH--- 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57
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                                                                                                                                                                                                                     ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 APOAPPAP-----PAQAQAQAPAQAQEAPAPQRSRGADTRALTQVLFGELKGLAPG 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 SPEHPGSPGCMGPITCCTARTQCEAPATGPDLPHPGPDGHLDTHS.....SLSSN 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RSPTTAEIAEPLPITEEEV----LSCIEAGRSY------HATSLEAAQEGDGLP 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FÖPEPGV---QFPTFAMPTVVGEIXBYFROMVPTVHVRRAUBLAVQVNSATEDLTTAFG 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EE----MICEPPPALOEYIGLLYAIPCVPPSREELDFLTRPELREAFGCLRAGQYPRALE 206
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                                                                                                                    20005-3918
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                                                                                                                                                                             Washington
                                                                                                                                                            DC
                                                                                                                                                                                              E: Pillsbury Madison & Sutro, L.L.P. 1100 New York Avenue, N.W.
                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                            Young, Douglas B.
                                                                                                                                                                                                                                                                                                                                                             Zhang, Ying
                                                                                                                                                                                                                                                                                                                                                                                                     Bishai,
                     Word Perfect
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 9%; Score 81; DB 2; Length 287, 21.2%; Pred. No. 0.97;
                                                                                                                                                                                                                                                                                                                                                                                                     William R.
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US-08-533-306A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Patent No. 5837457
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4.9%; Score 81; DB 3; Length 287;
Best Local Similarity 21.2%; Pred. No. 0.97;
Matches 66; Conservative 38; Mismatches 108; Indels 100; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Strept
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PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/622,353
                                                                                                                                                                                                                                                                                         APPLICANT: Liu, Pu
APPLICANT: Collins, Francis S.
APPLICANT: Siciliano, Michael J.
APPLICANT: Claxton, David
TITLE OF INVENTION: Markers for I
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FILING DATE: 27-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
                                                                                        COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                164 RSPTTAEIAERLRITEEEV-----LSCIEAGRSY-------HATSLEAAQEGUGLP 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 EE----MICERFRALQEYLGINYATROVPRSREETLEFUTPPELREARGOLFAGGYPRALE 206
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                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
GPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                         STREET: P.O. EC. CITY: Bloomfield Hills
                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                          ADDRESSEE:
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SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                            ZIP: 48303
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Search completed: April 20, 2003, 14:08:21
Job time : 21 secs
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TELEFAX: (810) 641-0270
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 816 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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NAME: Smith, Deann F.
REGISTRATION NUMBER: 36683
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APPLICATION NUMBER: US/08/53,306A
FILING DATE: September 25, 1995
CLASSIFICATION: 435
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                                                                                              622 ELEKEQ 627
                                                                                                                                                                                                                                             234 LLCHRULDRPAEAFAAGERALQ----RLQAREGHRYYAPLLDAMVKLAYALGKDFVTLQE 289
                                                                                                                                                                                                                                                                                                                                                                                              473 ORQLHEYETELEDERNERALAAAAKKKLEGDLKDLELQADSAIKGREEAIKQLRKLQAQM 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  413 RALETOMBEMKTQLEELEDELQASEDAKLELEVNMQALKGQFEPDLQAPDEQNFEFREQL 472
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                                                                                                                                                290 RLEESO 295
                                                                                                                                                                                             585 DIEKERLAEELASSISCHNALQDEKRRIEAR
                                                                                                                                                                                                                                                                                            533 KDFORELED- ARASPDETFATAKENE-KKAKSLEADLMOLOEDL----AAAERARKOA 584
                                                                                                                                                                                                                                                                                                                                                                                                                                             162 QEYL-- --- 176
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                                                                                                                                                                                                                                                                                                                                      SREFIDELTREELREAFGCLKAGGYEPALELLLEVLEUGEKLTAHCPAAAVEALCAV 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRWKHVKLLF -----EIASARIEERKVSKFVVYQIIVIQTGSFDNNKAVLERRYSD 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---VEFPRKHLTGNFAEEMIC-----ERRRAL 161
                                                                                                                                                                                             IACLEE 621
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